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Run
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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1: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*

2: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT:*

3: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT:*

4: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT:*

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14.159 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd
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AAB17485
AAW35231
AAB17482
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AAW35152
AAW82847
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·Leu/Lys diastereom Leu/Lys diastereom Antipathogenic pep Diastereomer pepti Antipathogenic pep Diastereomer pepti Antipathogenic pep
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45	44	43	42	41	40	39	38	37	36	35	34	ω ω	3 2	ω H	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12
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16	16	15	14	14	28	15	73	153	21	21	14	13	13	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	77	77	37	14
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AAR67798	AAR67797	AAR56957	AAB17122	AAR67795	AAP91335	AAW77384	AAB52057	AAY29393	AAB60066	AAU03187	AAW82855	AAB17484	AAW35232	AAB17422	AAB17421	AAB17420	AAB17417	AAB17414	AAW82887	AAW82886	AAW82885	AAW82857	AAW82851	AAW82848	AAW35171	AAW35170	AAW35169	AAW35153	AAW35150	AAW82859	AAW82858	AAW77378	AAW82854
Monoamine derivati	Bisamine derivatiz	Peptide which neut	Calmodulin antagon	Antimicrobial olig		Lytic peptide with		Sperm whale myoglo	KL3 membrane activ	æ	Antipathogenic pep	Antipathogenic pep	m										рe	Antipathogenic pep	Leu/Lys diastereom		Leu/Lys diastereom		diaste		Antipathogenic pep	*	Antipathogenic pep

ALIGNMENTS

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RESULT
AAW35149
Leu/Lys diastereomer peptide; infection; therapy; excitatory neurotoxin; Honey bee venom; pardaxin; cytolytic activity; cancer; non-haemolytic; preservative; agricultural produce; bacterial cell lysis; agricultural pesticide; cell wall lysis.
                                                                                                     Misc-difference
                                                                                                                        Misc-difference
                                                                                                                                           Misc-difference
                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                      Leu/Lys diastereomer
                                                                                                                                                                                                                                                         14-APR-1998 (first entry)
                                                                                                                                                                                                                                                                            AAW35149;
                                                                                                                                                                                                                                                                                             AAW35149 standard; peptide;
20-FEB-1997;
                                                                Modified-site
                                                                                  Misc-difference
                 28-AUG-1997.
                                    WO9731019-A2
97WO-IL00066.
                                                                                                      /note=
8
                                                                                                                                           Location/Qualifiers
                                                                                    10
                                                                                                                                 /note= "D-form residue"
                                                       'note=
                                                                         note-
                                                                                             'note=
                                                                                                                                                                                                                                     peptide [D]-L3,4,8,10-K4L8.
                                                       "C-terminal amide"
                                                                          "D-form residue"
                                                                                            "D-form residue"
                                                                                                               "D-form residue"
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ARASS152
ID AAW35152
ID AAW35152
ID AAW3
XX AAW3
XX Leu
DE Leu
CKW Honn
KW Honn
KW AON
NKW ASTR
XX Synth
XX Synth
XX Key
FT Misc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents a Leu/Lys diastereomer peptide of the invention. The peptides of the invention have: (a) cytolytic activity on CC invention. The peptides of the invention have: (a) cytolytic activity on CC pathogenic cells (pathogens and malignant cells not naturally present in CC the body); but (b) no haemolytic activity, or such activity only at a concentration significantly higher than that at which they lyse pathogens. The peptides, their complexes and mixtures are used to treat CC infections (caused by bacteria, fungi, protozoa, mycoplasma or viruses) or cancer, in human and veterinary medicine. Also, they can be used as agricultural pesticides. The absence of haemolytic activity (associated with disturbance of alpha helical structures) means that the peptides thave few if any toxic effects, and those that include D-aa will have conceased resistance to proteolytic degradation. Non-haemolytic, cytotoxic random copolymers of pardaxin, each has a specific spectrum of activity, allowing selection of agents for particular applications. Since these random copolymers induce total lysis of bacterial cell walls, cresistance to them is unlikely to develop.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 12; Conservative 0
                                                                                                                                                                                                                                                       Synthetic
                     Misc-difference
                                                          Misc-difference
                                                                                                       Misc-difference
                                                                                                                                                  Misc-difference
                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                               Leu/Lys diastereomer peptide; infection; therapy; excitatory neurotoxin; Honey bee venom; pardaxin; cytolytic activity; cancer; non-haemolytic; preservative; agricultural produce; bacterial cell lysis; agricultural pesticide; cell wall lysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW35152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 21; Page 39; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide(s) having selective cytolytic activity - against pathogens and malignant cells, but no haemolytic activity, used for treating infections and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-APR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW35152 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (YEDA ) YEDA RES & DEV CO LTD
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                                                                                                                                                                                                                                                                                                                                                                                                          Leu/Lys diastereomer peptide [D]-K1,5,9,12L2,6,7,11-K4L8.
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                       /note= "D-form residue"
                                                                                                                                               /note= "D-form residue"
                                                                                                                                                                                             Location/Qualifiers
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/note= "D-form residue
                                                                                  "D-form
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Pred. No. 0.053;
; Mismatches 0; Indels
                                                                                                                          residue'
                                                                                  residue'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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AAW82847
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This sequence represents a Leu/Lys diastereomer peptide of the cinvention. The peptides of the invention have: (a) cytolytic activity on the peptides of the invention have: (a) cytolytic activity on the peptides of the invention have: (a) cytolytic activity on the peptides of the invention that all snot naturally present in the body); but (b) no haemolytic activity, or such activity only at a concentration significantly higher than that at which they lyse concentrations (caused by bacteria, fungi, protoxo, mycoplasma or viruses) are used to treat to infections (caused by bacteria, fungi, protoxo, mycoplasma or viruses) or cancer, in human and veterinary medicine. Also, they can be used as preservatives for food, cosmetics and agricultural produce, or as agricultural pesticides. The absence of haemolytic activity (associated with disturbance of alpha-helical structures) means that the peptides thave few if any toxic effects, and those that include D-aa will have concreased resistance to proteolytic degradation. Non-haemolytic, cytotoxic random copolymers of pardaxin, each has a specific spectrum of activity, allowing selection of agents for particular applications. Since these tandom copolymers induce total lysis of bacterial cell walls, cresistance to them is unlikely to develop.
                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 12; Conservative (
Non-hamolytic; cytolytic; selective cytolytic activity; pathogen; cancer; infection; disinfectant; contact lens wetting solution; preservative; pesticide; fungicide; bactericide.
                                                                                                              19-MAY-1999
                                                                                                                                                                                      AAW82847 standard; peptide; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 21; Page 40; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oren Z,
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Misc-difference 11
                                                                         Antipathogenic peptide.
                                                                                                                                                     AAW82847
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide(s) having selective cytolytic activity - against pathogens and malignant cells, but no haemolytic activity, used for treating infections and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-435088/40.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acid residues and/or D-amino acid residues and comprises an alpha-helix breaker molety, or a peptide (or cyclic derivative of this) which (comprises L-amino acid residues and D-amino acid residues, has a net positive charge greater than I and has an amino acid sequence such that a corresponding amino acid sequence comprising only L-amino acid residues is not found in nature. The cytolytic agents may be used for treatment of cancer or for treatment of several diseases caused by pathogens, including bacterial, fungal, viral, mycoplasma and protozoan infections. They may be used in both human and veterinary medicine. They may also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present peptide is used to produce the agents of the invention. The specification describes a non-haemolytic, cytolytic agent, which is a peptide, a complex of bundled peptides, a mixture of peptides or a random peptide copolymer. The agent has a selective cytolytic activity on pathogenic cells. The agent is selected from a cyclic derivative of a peptide which has a net positive charge greater than 1, comprises 1-amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New non-haemolytic cytolytic agent useful in treating cancer infections - is a peptide comprising a moiety which disrupts continuity of an alpha-helical structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 12; Page 105; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-594464/50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  solutions for wetting contact lenses, as preservatives, e.g., cosmetic and food industries, as pesticides (e.g. fungicides bactericides) or for preservation of agricultural products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-FEB-1997;
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27-AUG-1998
                               WO9837090-A1
                                                                Synthetic
                                                                                               cancer; infection; disinfectant; contact lens we
preservative; pesticide; fungicide; bactericide.
                                                                                                                                Non-haemolytic; cytolytic; selective cytolytic activity; pathogen;
                                                                                                                                                               Antipathogenic peptide
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                                                                                                                                                                                                                                                                                                                                                     klllklllkllk 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 as disinfectants for destruction of microorganisms, i.e. i
                                                                                                                                                                                                                                                                                                                                                                                                                     12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12
                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98WO-IL00081
                                                                                                                                                                                                                                                                peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                     .0%;
                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 52; DB 19 Pred. No. 0.053; Mismatches
                                                                                                                contact lens wetting solution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   0
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the
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AAW82856
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Best Local S
Matches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            breaker molety, or a peptide (or cyclic derivative of this) which (comprises L-amino acid residues and D-amino acid sequence such that positive charge greater than 1 and has an amino acid sequence such that a corresponding amino acid sequence comprising only L-amino acid residues is not found in nature. The cytolytic agents may be used for treatment of several diseases caused by pathogens, including bacterial, fungal, viral, mycoplasma and protozoan infections. They may be used in both human and veterinary medicine. They may also be used as disinfectants for destruction of microorganisms, i.e. in solutions for wetting contact lenses, as preservatives, e.g., in the cosmetic and food industries, as pesticides (e.g. fungicides or bactericides) or for preservation of agricultural products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present peptide is used to produce the agents of the invention. The specification describes a non-haemolytic, cytolytic agent, which is a peptide, a complex of bundled peptides, a mixture of peptides or a random
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 13; Page 106; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-594464/50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oren
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide copolymer. The agent has a selective cytolytic activity on pathogenic cells. The agent is selected from a cyclic derivative of a peptide which has a net positive charge greater than 1, comprises L-amino acid residues and/or D-amino acid residues and comprises an alpha-helix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      continuity of an alpha-helical structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New non-haemolytic cytolytic agent useful in treating cancer or infections - is a peptide comprising a moiety which disrupts the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                              19-FEB-1998;
                                                                               27-AUG-1998
                                                                                                                W09837090-A1
                                                                                                                                             Synthetic
                                                                                                                                                                                preservative;
                                                                                                                                                                                                cancer;
                                                                                                                                                                                                             Non-haemolytic;
                                                                                                                                                                                                                                              Antipathogenic peptide.
                                                                                                                                                                                                                                                                                 19-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                  AAW82856;
                                                                                                                                                                                                                                                                                                                                               AAW82856 standard; peptide; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KLLLKLLKLLK 12
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| 1 klllklllkllk 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity
12; Conser
                                                                                                                                                                                                infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                pesticide; fungicide; bactericide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97WO-IL00066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98WO-IL00081
                                                98WO-IL00081
                                                                                                                                                                                              cytolytic; selective cytolytic activity; pathogen; on; disinfectant; contact lens wetting solution;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 52; DB 19; Pred. No. 0.053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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0;

20-FEB-1997;

97WO-IL00066

Oren

cancer and

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The present peptide is used to produce the agents of the invention. The CS specification describes a non-haemolytic, cytolytic agent, which is a CC peptide, a complex of bundled peptides, a mixture of peptides or a random CC peptide copolymer. The agent has a selective cytolytic activity on pathogenic cells. The agent has a selected from a cyclic derivative of a comprises in a comprise of a peptide which has a net positive charge greater than 1, comprises in a light helix comprises of a peptide (or cyclic derivative of this) which comprises the comprise of the comprises of the comprises of the comprise of the comprises of the comprises of the comprise of the cyclic derivative of this pations of the cyclic derivative of the cyclic derivative of the cyclic of comprises of the cyclic derivative and sequence such that a corresponding amino acid sequence comprising only in a cid residues of a corresponding amino acid sequence comprising only in a cyclic derivative of the cyclic agents may be used for treatment of contact agents and protozoan infections. They may be used in both human and veterinary medicine. They may also be solutions for wetting contact lenses, as preservatives, e.g., in the committee of the cyclic derivative, as posticides (e.g. fungicides or bactericides) or for preservation of agricultural products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoinmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPG; FPG; CTLA4; minetic; IL-1; TMP; antagonist; immunosuppressive; EPG; FPG; CTLA4; minetic; IL-1; TMP; antagonist; immun; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                23-OCT-1998;
22-OCT-1999,
                                                                                                                                                                        25-OCT-1999;
                                                                                                                                                                                                                                                     04-MAY-2000
                                                                                                                                                                                                                                                                                                                                 WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New non-haemolytic cytolytic agent useful in treating cancer or infections - is a peptide comprising a moiety which disrupts the continuity of an alpha-helical structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antipathogenic peptide sequence SEQ ID NO:517.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB17413 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (YEDA )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KLLLKLLLKLLK 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 100.0%;
1 Similarity 100.0%;
12; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YEDA RES & DEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12
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                                                98US-0105371
99US-0428082
                                                                                                                                                                        99WO-US25044
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 52; DB 19;
Pred. No. 0.053;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
AAB17416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes composition of matter (1) comprising an CC FC domain, pharmacologically active peptides, and linkers. Where (1) is: CC (X1)a*F1*(X2)b, where: F1 = an FC domain; X1 and X2 = are each (X1)a*F1*(X2)b, where: F1 = an FC domain; X1 and X2 = are each (CC (F1)c-F1*(L2)d*F2*(L3)c-F1*(L2)d*F2*(L3)c-F1*(L2)d*F2*(L3)c-F1*(L2)d*F2*(L3)c-F1*(L2)d*F2*(L3)c-F1*(L2)d*F2*(L3)c-F1*(L2)d*F2*(L3)c-F1*(L2)d*F2*(L3)c-F1*(L2)d*F2*(L3)c-F1*(L2)d*F2*(L3)c-F1*(L2)d*F2*(L3)c-F1*(L2)d*F2*(L3)c-F1*(L2)d*F2*(L3)c-F1*(L2)d*F2*(L3)c-F1*(L2)d*F2*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(L3)c-F1*(
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Best Local S
Matches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; minetic; IL-1; TMP; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                      23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                         25-OCT-1999;
                                                                                                                                                                                                                                                                                      04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antipathogenic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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         (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                   WO200024782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Feige U, Liu C, Cheetham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AMGE-) AMGEN INC
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                                                                                      98US-0105371
99US-0428082
                                                                                                                                                                                                         99WO-US25044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide sequence SEQ ID NO:520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J, Boone TC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 52; DB 21;
Pred. No. 0.053;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fc domain and for treating
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0;

0; Gaps

0;

Length 12; Indels

g Qy

6

RESULT AAB17413 XX AAB1 XX AAB1 XX AAB1 XX AAB1 XX AAB1 XX MOdi XX Modi XX Modi XX Modi XX Limnu XW Limnu XW WARP; XX OSYLC XX OSYLC XX D3-C YX D3-C Y

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RESULT E
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CC (X1)a+F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each

CC independently selected from -(L1)c-P1 -(L2)d-P2 -(L2)d-P2.

CC (L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4

CC where P1, P2, P3, and P4 = are each independently sequences of

CC pharmacologically active peptides; L1, L2, L3, and L4 = are each independently

CC independently linkers; and a, b, c, d, e, and f = are each independently

CC or 1, provided that at least 1 of a and b is 1. The composition can

CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive

CC activities. DNas, vectors and host cells from the present invention can

CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.

CC The use of an Fc domain (rather than a Fab domain) can provide a longer

CC half-life or incorporate functions such as Fc receptor binding, protein

CC h binding, complement fixation, and possibly placental transfer. AAA69443

CC constant of the procession of the present invention acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                           23-OCT-1998;
22-OCT-1999;
                                                                                                                                                 WO200024782-A2
                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                          cytotoxic T cell lymphocyte antigen vascular endothelial growth factor;
                                                                                                                                                                                                                                                   Modified peptide; therapeutic agent; fusion; Fc domain; cance autoimmune disease; Cytostatic; antiasthmatic; thrombolytic; immunosuppressive; EPO; TPO; CTLA4; mimetic; II-1; TNF; anta MMPH; inhibitor; erythropoietin; thrombopoietin; interleukin
                                                                                                                                                                                                                                                                                                                                                               31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Feige
                                                                                                                     04 - MAY - 2000
                                                                                                                                                                                                             asthma;
                                                                                                                                                                                                                                                                                                                              Antipathogenic peptide sequence SEQ
                                                                                                                                                                                                                                                                                                                                                                                             AAB17483;
                                                                                                                                                                                                                                                                                                                                                                                                                         AAB17483 standard; Peptide; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequences used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes composition of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pharmacologically active
              (AMGE-) AMGEN
                                                                                       25-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KLLLKLLKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                composition of matter comprising an accologically active peptides, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ü
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39; Page 379; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity
12; Conser
                                                                                                                                                                                                               thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ç
                                           98US-0105371
99US-0428082
                                                                                       99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cheetham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 52;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Boone
                                                                                                                                                                                                                                      thrombopoietin; interleukin 1; igen 4; tumour necrosis factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                 ID NO:587.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fc domain and
for treating
                                                                                                                                                                                                                                                                                                   Fc domain; cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           matter (I) comprising and linkers. Where (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12;
                                                                                                                                                                                                                                                                      antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC (XI)a-FI-(X2)b, where: FI = an Fc domain; XI and XI = are each (XI)a-FI-(X2)b, where: FI = an Fc domain; XI and X2 = are each (XI)a-FI-(X2)b-P2-(XI)e-P3-(XI)c-P1-(XI)d-P2-(XI)d-P2-(XI)e-P3-(XI)e-P3-(XI)d-P2-(XI)d-P2-(XI)d-P2-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)d-P2-(XI)d-P2-(XI)d-P2-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-(XI)e-P3-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MMP; inhibitor; erythropoietin; thrombopoietin; interle cytotoxic T cell lymphocyte antigen 4; tumour necrosis vascular endothelial growth factor; matrix metalloprote asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel composition of matter comprising an pharmacologically active peptides, useful
                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; MMP; inhibitor; erythropoietin; thrombopoietin; interle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified peptide; therapeutic agent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antipathogenic peptide sequence SEQ ID NO:589.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB17485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB17485 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Feige U,
                                                                                                                         23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                        25-OCT-1999;
                                                                                                                                                                                                                                                                                         04-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                         WO200024782-A2
                                                            (AMGE-) AMGEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity
12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                         98US-0105371
99US-0428082
                                                                                                                                                                                                                            99WO-US25044
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           608pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 52;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Boone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antiasthmatic; thrombolytic; VEGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        matrix metalloproteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fusion; Fc domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        interleukin 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (I) comprising (ers. Where (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is
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0,

Feige U,

Liu C,

Cheetham J,

Boone

TC;

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RESULT
AAW35231
ID AAW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes composition of matter (I) comprising an CC (XI)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 (L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 (L2)d-P2-(L3)e-P3-(L4)f-P4 (L2)d-P2-(L3)e-P3-(L4)f-P4 (L2)d-P2-(L3)e-P3-(L4)f-P4 (L2)d-P2-(L3)e-P3-(L4)f-P4 (L2)d-P2-(L3)e-P3-(L4)f-P4 (L2)d-P2-(L3)e-P3-(L4)f-P4 (L3)e-P3-(L3)e-P3-(L4)f-P4 (L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                    20-FEB-1997;
                                                                                            28-AUG-1997.
                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Diastereomer peptide; infection; therapy; excitatory neurotoxin; Honey bee venom; pardaxin; cytolytic activity; cancer; non-haemolytic; preservative; agricultural produce; bacterial ceagricultural pesticide; cell wall lysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer autoimmune diseases -
                                                                                                                                                WO9731019-A2
                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Diastereomer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 39; Page 402; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-350702/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW35231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW35231 standard; peptide; 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity es 12; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 kliikliiklik 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KLLLKLLKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide [D]-L3,4,8,10-K4L8C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                         /note=
                                    97WO-IL00066
                                                                                                                                                                                                                          /note=
                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                    /note=
                                                                                                                                                                                                                                                                                                             /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; s
100.0%; s
tive 0;
                                                                                                                                                                                                 "D-form residue
                                                                                                                                                                                                                                                                                                          "D-form
                                                                                                                                                                                                                                                         "D-form
                                                                                                                                                                                                                                                                                                                                                                 "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 52; DB 21;
Pred. No. 0.053;
; Mismatches 0;
                                                                                                                                                                                                                                                      residue
                                                                                                                                                                                                                                                                                                             residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bacterial cell lysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
   AC XXX AC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB17482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC sequence represents a diastereomer peptide of the invention. This CC sequence is used in a "bundle sequence", which is created by binding 5 CC copies of this sequence to peptide 23 (see ANM35149). The peptides of CC copies of this sequence to peptide 23 (see ANM35149). The peptides of CC and malignant cells not naturally present in the body; but (b) no CC haemolytic activity, or such activity only at a concentration CC significantly higher than that at which they lyse pathogens. The CC peptides, their complexes and mixtures are used to treat infections CC (caused by bacteria, fungi, protozoa, mycoplasma or viruses) or cancer, CC in human and veterinary medicine. Also, they can be used as preservatives CC for food, cosmetics and agricultural produce, or as agricultural CC disturbance of alpha-helical structures) means that the peptides have few CC disturbance of alpha-helical structures) means that the peptides have few CC if any toxic effects, and those that include D-aa will have increased CC resistance to proteolytic degradation. Non-haemolytic, cytotoxic random CC copolymers of pardaxin, each has a specific spectrum of activity. CC allowing selection of agents for particular applications. Since these CC random copolymers induce total lysis of bacterial cell walls, resistance CC contents is unitkely to develow.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                       Modified peptide; therapeutic agent; fusion; Fc domain; cancer autoimmune disease; cytostatic; antiasthmatic; thrombolytic; V immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TLR; antago MMP; inhibitor; erythropoletin; thrombopoletin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
23-OCT-1998;
                                                    25-OCT-1999;
                                                                                                           04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB17482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB17482 standard; Peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide(s) having selective cytolytic activity - against pathogens and malignant cells, but no haemolytic activity, used for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-435088/40.
                                                                                                                                                               WO200024782-A2
                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                        asthma; thrombosis; pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antipathogenic peptide sequence SEQ ID NO:586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to them is unlikely to develop.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 7; Page 49; 80pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (YEDA ) YEDA RES & DEV CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                infections and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KLLLKLLKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity
12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; ilarity 100.0%; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                    99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96IL-0117223.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 52; DB 18
Pred. No. 0.057;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 13;
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Indels

0; Gaps

0;

antagonist;

22-OCT-1999;

99US-0428082

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RESULT :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fc domain, pharmacologically active peptides, and linkers. Where (I) is:

(Xl)a-Fl-(X2)b, where: Fl = an Fc domain; Xl and X2 = are each

independently selected from -(Ll)c-Pl, -(Ll)d-Pl-(L3)d-P2.

(Ll)c-Pl-(L2)d-P2-(L3)e-P^3, or -(Ll)c-Pl-(L2)d-P2-(L3)e-P3-(L4)f-P4

where Pl, P2, P3, and P4 = are each independently sequences of

pharmacologically active peptides; Ll, Li2, Li3, and Li4 = are each independently

clindependently linkers; and a, b, c, d, e, and f = are each independently

clindependently linkers; and a, b, c, d, e, and f manunosuppressive

activities. DNAs, vectors and host cells from the present invention can

be used for producing pharmaceutical compositions. The compositions are

useful for treating cancer, asthma, thrombosis, or autoimmune diseases.

The use of an Fc domain (rather than a Fab domain) can provide a longer

half-life or incorporate functions such as Fc receptor binding, protein

A binding, complement fixation, and possibly placental transfer. AAA6943

to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel composition of matt pharmacologically active autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 39; Page 401; 608pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-350702/30.
                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                         Non-haemolytic; cytolytic; selective cytolytic activity; pathogen; cancer; infection; disinfectant; contact lens wetting solution;
                                                                                                                                                                                                                                                                      Antipathogenic
                                                                                                                                                                                                                                                                                                                                                          AAW82854 standard; peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AMGE-) AMGEN INC
                                        (YEDA ) YEDA RES & DEV CO LTD
                                                                                               19-FEB-1998;
                                                                                                                           27-AUG-1998
                                                                                                                                                       W09837090-A1
                                                                                                                                                                                                             preservative;
                                                                                                                                                                                                                                                                                                   19-MAY-1999
                                                                                                                                                                                                                                                                                                                                AAW82854;
                                                                                                                                                                                                                                                                                                                                                                                       12
                                                                                                                                                                                                                                                                                                                                                                                                                                  Н
                                                                                                                                                                                                                                                                                                                                                                                                                               KLLLKLLKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention describes composition of matter (I) comprising
                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ç
                                                                                                                                                                                                             pesticide; fungicide;
                                                                    97WO-IL00066
                                                                                                                                                                                                                                                                    peptide
                                                                                               98WO-IL00081.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        matter comprising an tive peptides, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 52; DB 21
Pred. No. 0.057;
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                                                                                                                                                                                                              bactericide.
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밁 Q

Sequence

14

AA,

₽B 19;

Length 14;

0

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cancer or for treatment of several diseases caused by pathogens, including bacterial, fungal, viral, mycoplasma and protozoan infections. They may be used in both human and veterinary medicine. They may also be used as disinfectants for destruction of microorganisms, i.e. in solutions for wetting contact lenses, as preservatives, e.g., in the cosmetic and food industries, as pesticides (e.g. fungicides or bactericides) or for processing of sample and products.
                                                                                                                                                                                                                                           acid residues and/or D-amino acid residues and comprises an alpha-helix breaker modety, or a peptide (or cyclic derivative of this) which (comprises L-amino acid residues and D-amino acid residues, has a net positive charge greater than 1 and has an amino acid sequence such that a corresponding amino acid sequence comprising only L-amino acid residues is not found in nature. The cytolytic agents may be used for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                specification describes a non-haemolytic, cytolytic agent, which is a peptide, a complex of bundled peptides, a mixture of peptides or a random peptide copolymer. The agent has a selective cytolytic activity on pathogenic cells. The agent is selected from a cyclic derivative of a peptide which has a net positive charge greater than 1, comprises L-amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New non-haemolytic cytolytic agent useful in treating cancer or infections - is a peptide comprising a moiety which disrupts the continuity of an alpha-helical structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-594464/50
                                                 cosmetic and food bactericides) or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present peptide is used to produce the agents of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 14; Page 106; 126pp; English.
                                                    for preservation of agricultural
                                                       products.
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AAW77378
                                                                                                                                                                                                                                                                                                                     RESULT
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                           Biologically a
lipid bilayer
                                                  18-MAR-1997;
                                                                         18-MAR-1998;
                                                                                                                           W09841535-A2
                                                                                                                                                   Synthetic
                                                                                                                                                                                                                 Lytic peptide
                                                                                                                                                                                                                                            14-DEC-1998
                                                                                                                                                                                                                                                                   AAW77378;
                                                                                                                                                                                                                                                                                           AAW77378 standard; peptide; 37
Ajoula
                       (ANMA-) ANMAT TECHNOLOGY LTD
                                                                                                 24-SEP-1998
                                                                                                                                                                                                                                                                                                                    13
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Local Similarity 100.0%;
les 12; Conservative 0
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HS,
Clarke DJ
                                                                                                                                                                          active peptide; hormone; drug; toxin;
r membrane; microorganism; parasite; v
                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                 with alterable function
                                                  97GB-0005519
                                                                        98WO-GB00799
                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 52;
Pred. No.
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A CONTROL OF THE CONT

acids which

are not to

be modified

New modified peptide(s) - obtained by substitution with an amino acid which is modifiable by a reaction and replacing other amino

Claim 7;

Page

33pp; English

8x35555555555555

The peptides AAW77376-W77390 can be modified by the method of the period invention by substituting at least one amino acid of the peptide to provide a peptide having at least one amino acid which is modifiable by a reaction and replacing other amino acids in the peptide with amino acids which are not modifiable by the reaction. The methods can be used for the modification of biologically active peptides such as hormones, toxins and peptides which act on lipid bilayer membranes. The modified peptides can be used e.g. in the body of an animal or plant or parts in order to affect the structure or integrity or permeability of a foreign body such as a microorganism, parasite or virus present in the body of the animal or plant or within the cells of the body of the animal

Ъ Qy

11

22

1 KLLLKLLKLLK

12;

Conservative

Similarity

100.0%; 0;

Score 52; Pred. No.

0.16; DB 19; 0,

Length 37; Indels

0,

0;

Mismatches

14

Query Match Best Local Matches

Sequence

37

AA;

plant

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RRESULT 1
AAMW6284
XX AAW62
XX AAW6
XX AAW6
XX Non
XX Non
XX VOOR
XX V
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specification describes a non-haemolytic, cytolytic agent, which is a specification describes a non-haemolytic, cytolytic agent, which is a peptide, a complex of bundled peptides, a mixture of peptides or a random peptide copolymer. The agent has a selective cytolytic activity on pathogenic cells. The agent is selected from a cyclic derivative of a pathogenic cells. The agent is selected from a cyclic derivative of a cid residues and/or D-amino acid residues and comprises an alpha-helix breaker moiety, or a peptide (or cyclic derivative of this) which breaker moiety, or a peptide (or cyclic derivative of this) which positive charge greater than 1 and has an amino acid sequence such that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New non-haemolytic cytolytic agent useful in treating cancer infections - is a peptide comprising a moiety which disrupts continuity of an alpha-helical structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 17; Page 106; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (YEDA ) YEDA RES & DEV CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-594464/50
                                                                                                                                                                                                                                                                                                                                                              present peptide is used to produce the agents of the invention. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; peptide;
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RESULT
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The present peptide is used to produce the agents of the invention. The cspecification describes a non-haemolytic, cytolytic agent, which is a cc peptide, a complex of bundled peptides, a mixture of peptides or a random cc peptide copolymer. The agent has a selective cytolytic activity on cc peptide which has a net positive charge greater than 1, comprises L-amino cc peptide which has a net positive charge greater than 1, comprises L-amino ccid residues and/or D-amino acid residues and comprises an alpha-helix c comprises L-amino acid residues and D-amino acid residues, has a net c (comprises L-amino acid residues and D-amino acid residues, has a net c positive charge greater than 1 and has an amino acid sequence such that positive charge greater than 1 and has an amino acid sequence such that corresponding amino acid sequence comprising only L-amino acid residues a corresponding amino acid sequence comprising only L-amino acid residues a corresponding amino acid sequence comprising only L-amino acid residues including bacterial, fungal, viral, mycoplasma and protozoan infections. They may be used in both human and veterinary medicine. They may also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Non-haemolytic; cytolytic; selective cytolytic activity; pathogen; cancer; infection; disinfectant; contact lens wetting solution; preservative; pesticide; fungicide; bactericide.
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                                                                                                                                                                                                                                                                                                                                   New non-haemolytic cytolytic agent useful in treating cancer or infections - is a peptide comprising a moiety which disrupts the continuity of an alpha-helical structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (YEDA ) YEDA RES & DEV CO LTD
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                                                                                                                                                                                                                                                                                                  Claim 17; Page 107; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-594464/50
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12; Conserv
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Pred. No.
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CC used as disinfectants for destruction of microorganisms, i.e. in CC solutions for wetting contact lenses, as preservatives, e.g., in the CC cosmettic and food industries, as preservatives (e.g. fungicides or CC bactericides) or for preservation of agricultural products.

XX

SQ Sequence 77 AA;

Ouery Match 100.0%; Score 52; DB 19; Length 77; Best Local Similarity 100.0%; Pred. No. 0.33; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Indels 12; Conservative 0; Mismatches 0; Indels 0; Gaps O; Indels O; Indels O; Gaps O; Indels O; Gaps O; Indels O; Indels O; Indels O; Indels O; Indels O
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GenCore version 4.5
Copyright (c) 1993 - 2000 Com
  Compugen Ltd
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OM protein protein search, using sw model

Run on:

June 17, 2002, 12:38:45; Search time 46.42 Seconds (without alignments)
24.840 Million cell updates/sec

Scoring table: Sequence: Perfect score: US-09-367-714A-23 BLOSUM62 1 KILLKLLKLLK 12

Title:

Gapop 10.0 , Gapext 0.5

283138 seqs, 96089334 residues

Searched:

Total number of hits satisfying chosen parameters:

283138

Minimum DB Maximum DB seq length: 0
seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

Database PIR_71:* pir2:*
pir3:*

and is score No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	σ	4	ω	2	_	No.	Result
33	33	33	33	34	34	34	34	34	34	34	34	34	34	34	34	34	34	35	35	35	35	36	36	37	37	37	37	40	Score	•
63.5	ω.	ω ·	·	65.4	ر.	65.4	65.4	65.4	65.4	65.4	65.4	65.4	65.4	65.4	65.4	65.4	65.4	67.3	67.3	67.3	67.3	•		71.2	71.2	71.2	71.2	76.9	Match	Query
144	109	91	84	1712	986	984	707	662	662	552	433	282	235	235	213	191	53	3268	319	318	39	1896	143	465	255	238	137	2513	Length	
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T18867	S42121	G70155	E96916	C71618	T41809	DJNVCP	н82709	E97973	E95105	F71132	A69735	G71932	в97109	140627	T01464	F90392	T03171	S69625	A70102	C81386	G85837	T01490	S03747	T30155	A60637	E71375	A96914	G96536	ID	
hypothetical prote		•		hypothetical prote	DNA polymerase orf	DNA-directed DNA p	colicin V secretio	÷	ABC transporter, p	probable nitrite r	(D)	hypothetical prote	DNA-dependent RNA	3		hypothetical prote	μ.	hypothetical prote	conserved hypothet	(D)			_	hypothetical prote	merozoite antigen	probable ABC trans	ίz	etical pro	Description	

ALIGNMENTS

hypothetical protein F2J10.9 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: G96536
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
A.;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Reference number: A86141; MUID:21016719
A.;Accession: G96536
A.;Catatus, C.S. (1988) A. (1988

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-2513 <STO>

A;Cross-references: GB:AE005173; NID:g8569097; PIDN:AAF76442.1; GSPDB:GN00141

C; Genetics

A;Gene: F2J10.9

A; Map position: 1

Query Match Best Local Matches Local Similarity hes 10; Conserv Conservative 76.98; Score 40; DB 2; Le Pred. No. 1.1e+02; 0; Mismatches 1; Length 2513; Indels 0; Gaps

0;

밁 797 LLLGLLLKLLK 807 2 LLLKLLLKLLK 12

RESULT A96914 N

uncharacterized protein, Yje/RRF2 family [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 C;Accession: A96914 R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001 A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium A;Reference number: A96900; MUID:21359325; PMID:21359325

A; Title: Genome Sequence and A; Reference number: A96900; A; Accession: A96914

A; Status: preliminary

A; Molecule type: DNA A; Residues: 1-137 <KUR>

A;Cross-references: GB:AE001437; PIDN:AAK78100.1; PID:g15022941; GSPDB:GN00168

```
probable ABC transporter, ATP-binding protein - syphilis spirochete C; Species: Treponema pallidum subsp: pallidum (syphilis spirochete) C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 17-Mar-2000 C;Accession: E71375
C;Accession: E71375
R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, Teson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1988
A;Tille: Complete genome sequence of Treponema pallidum, the syphilis spirochete angel of the symphilis spirochete angel of the symphilis spirochete and the symphilis spirochete symphilis spirochete and the symphilis spirochete symphilis spiroch
                                                                                                                                                                                                                                                 A;Cross-references: GB:M30933
C;Keywords: tandem repeat
F;18-240/Region: glutamine-ric
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В
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                                                                                                                                                                                                                                                                                                                                                                                                 R:Ko, C.; Smith II, C.K.; McDonell, M.
Mol. Biochem. Parasitol. 41, 53-64, 1990
A;Title: Identification and characterization of a target antigen of a monoclonal antiboo A;Reference number: A60637; MUID:90348718
A;Accession: A60637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  merozoite antigen LPMC-61 - Eimeria tenella (fragment)
C;Species: Eimeria tenella
C;Decies: Eimeria tenella
C;Dete: 28-Apr-1933 #sequence_revision 28-Apr-1993 #text_change 07-May-1999
C;Accession: A60637
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A;Mosidues: 1-238 <COL>
A;Cross-references: GB:AE001188; GB:AE000520; NID:g33222
A;Experimental source: strain Nichols
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A; Residues: 1-255 < KOA>
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Best Local Similarity
Thes 8; Conserv
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Matches 8
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2 RLLLKLLLLLL
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                                                  1 KLLLKLLKLL 11
                                                                                                           9; Conservative
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8; Conser
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81.8%;
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Pred. No. 25;
2; Mismatches
                                                                                                           Score 37; DB 2; Pred. No. 44; 1; Mismatches
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                                                                                                           A; Cross-references: GB:299111;
A; Experimental source: strain
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                       A;Gene: eag
C;Superfamily: Bacillus
                                                                                C; Genetics:
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A; Residues: 1-143 <KUN>
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subtilis small membrane protein

GB:AL009126;

NID:g2633699; PIDN:CAB13238.1;

PID:g26337

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A;Cross.references: EMBL:Y00526; NID:940181; PIDN:CAA68584.1; PID:940183
A;Cross.references: EMBL:Y00526; NID:940181, A.M., Alloni, G., Azevedo, V.; Beron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A.; Ehrlich, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J.; Fabret, C.; Ferrari,
A.; Ehrlich, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J.; Fabret, C.; Ferrari,
A.; Ehrlich, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J.; Fabret, C.; Ferrari,
A.; Ehrlich, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J.; Fabret, C.; Ferrari,
A.; Ehrlich, S.; Galizzi, A.; Gal
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.
Koetter, P.; Koningstein, G.; Kcoph, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino
A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadafe, Y.; Sato, T.; Scanl
A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida
A; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili
A; Accession: C69619
A; Statis: Number: A69580; MUID:98044033
A; Statis: Number: A69580; Muid:98044033
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A;Molecule type: DNA
A;Residues: 1-465 <LETY
A;Residues: 1-465 <LETY
A;Cross-references: EMBL:U97194; PIDN:AAB52449.1; GSPDB:GN00019; CESP:C37A2.5
A;Cross-references: EMBL:U97194; PIDN:AAB52449.1; GSPDB:GN00019; CESP:C37A2.5
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Mol. Microbiol. 1, 125-132, 1987
A;Tille: Isolation and sequence of the spoOE gene: its role in initiation of A;Reference number: $03746; MUID:88260878
A;Accession: $03747
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C;Date: 21-Nov-1993 #sequence_revision 01-Dec-1995
C;Accession: S03747; C96619
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C;Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T30155
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A; Introns: 47/1; 117/1;
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A; Residues: 1-143 < PER>
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Pred. No.
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77;
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R:Vysotskaia, V.S.; Schwartz, J.R.; Toriumi, M.; Yu, G.; Kvrtz, D.; Li, Y.; Palm, C.J.; Shinn, P.; Sun, H.; Davis, R.P. submitted to the EMBL Data Library, June 1998
A:Description: Arabidopsis thaliana chromosome 1 BAC F1707
A:Reference number: Z14334
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A;Gene:
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A;Title: Genome sequence of enterohemorrhagic Escherichia coa;Reference number; A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a; molecule type: DNA
a; Residues: 1-1896 < VYS>
A; Cross-references: EMBL: ACC003671; NID: g2833627;
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C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
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A; Introns: 11/3; 43/3;
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A;Accession: G85837
A;Status: preliminary
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Best Local S
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                             LLLKLLKLLK 12
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MLLKLIKIFK 11
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8; Conserv
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                                                                                                                                                                               GB:AE005174; NID:g12516312; PIDN:AAG57163.1; ce: strain O157:H7, substrain EDL933
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Pred.
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                                                                              Score 35;
Pred. No.
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Pred. No.
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38;
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17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PID:g3176689; GSPDB:GN00059; ATSP:F170
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                                                                                               Length 39;
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RESULT

9

A; Molecule type: DNA

A; Accession: S69625

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probable integral membrane protein Cj0421c [imported] - Campylobacter jejuni C;Species: Campylobacter jejuni C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 31-Mar-2000 C;Accession: C81386 R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          conserved hypothetical integral membrane protein BB0017 - Lyme disease spirochete C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 29-Sep-1999 C;Accession: A70102 R;Fraser, C.M.; Casjens, B.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bowman, C.; Garland, S.; Fujil, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, Nature 390, 580-586; 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AL139075; GB:AL111168; NID:g6967817; PIDN:CAB74257.1; PID:g696A;Experimental source: serotype O2, strain NCTC 11168 C;Genetics: A;Gene: Cj0421c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C.W.; Quail, M.; Rajandream,
Nature 403, 665-668, 2000
R;Dietrich, F.S. submitted to the EMBL Data Library, August 1995 A;Description: The sequence of S. cerevisiae cos A;Reference number: S69554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE001116; GB:AE000783; NID:g2687896; A;Experimental source: strain B31 C;Superfamily: conserved hypothetical protein yitT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete,
A;Reference number: A70100; MUID:98065943
A;Accession: A70102
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A; Residues: 1-318 <PAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals A;Reference number: A81250; MUID:20150912
                                                                                                                      hypothetical protein YDR457w - yeast (Saccharomyces cerevisiae) C;Species: Saccharomyces cerevisiae C;Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change
                                                                                                                                                                                            RESULT
S69625
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Best Local
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Best Local Similarity
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58.3%;
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66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 35; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                    Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                            1.2e+02;
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                                    cosmids 9410,
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K.M.; VanVliet, A.;
                                                                                                                           #text_change
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                                    8035,
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                                                                                                                                23-Mar-2001
                                    8166, and 9787
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В 20

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probable antibiotic polypeptide - Chilo iridescent virus
C:Speckes: Chilo iridescent virus
C:Speckes: Chilo iridescent virus
C:Speckes: Chilo iridescent virus
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 20-Aug-1999
C:Accession: T03171
R:Bahr, U: Tidona, C.A.; Darai, G.
Virus Genes 15, 235-245, 1997
Virus Genes 15, 235-245, 1997
A:Title: The DNA sequence of Chilo iridescent virus between the genome coordinates 0.101
A:Reference number: Z14834; MUID:98141693
A:Accession: T03171
A:Status: prellminary; translated from GB/EMBL/DDBJ
A:Residues: 1-53 <BABL
A:Residues: 1-53 <BABL
A:Residues: 1-53 <BABL
A:Cross-Treferences: EMBE:AF003534; NID:g2738385; PIDN:AAB94469.1; PID:g2738442
C:Superfamily: s111ucin
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C,Genetics:
A,Gene: SGD:TON1
A,Cross-references: SGD:S0002865; MIPS:YDR457w
A,Map position: 4R
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Matches 7
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Best Local Similarity 88.
Matches 8; Conservative
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Best Local Similarity
Matches 8; Conserv
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3 ILLKILFKLL 12
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                                          LKALLKLLK 43
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88.9%;
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Pred. No. 1.1e
0; Mismatches
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Pred. No. 33;
2; Mismatches
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Pred. No. 9.9e+02;
1; Mismatches 0;
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No. 1.1e+02;
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R;Sauer, U; Treuner, A.; Buchholz, M.; Duerre, P.
R;Sauer, U; Treuner, A.; Buchholz, M.; Duerre, P.
R;Description: Sigma factor homologous genes in C. acetobutylicum.
A;Reference number: S34306
A;Accession: S34309
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 46-146, P/,148-235 <SAU>
A;Cross-references: EMBL:Z23079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable transcription initiation factor sigma E - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 15-Oct-1999 C;Accession: I40627; S34309 C;Accession: I40627; S34309 C;Accession: I40627; S34309 C;Accession: I40627; Sass, C.; Bennett, G.N. Gene 153, 89-92, 1995 A;Title: Sequence and arrangement of genes encoding sigma factors in Clostridi A;Accession: I40626; MUID:95189110 A;Accession: I40627; translated from GB/EMBL/DDBJ A;Molecula type: DNA A;Residues: 1-235 CRES-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein T24H24.20 ~ Arabidopsis thaliana (Species: Arabidopsis thaliana (Mouse-ear cress) c; Species: Arabidopsis thaliana (Mouse-ear cress) c; Date: 12:Feb-1999 #sequence_revisiton 12:Feb-1999 #text_change 24-Mar-1999 c; Date: 10:Feb-1999 #sequence_revisiton 12:Feb-1999 #text_change 24-Mar-1999 c; Accession: T01464

submitted to the EMBL Data Library, August 1998 A; Description: The sequence of A. thaliana T24H24.

A; Reference number: Z14333
A; Accession: T01464
A; Reference number: Z14333
A; Accession: T01464
A; Reference number: Z14333
A; Accession: T01464
A; Reference number: Z14333
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                                                                                                                                                                                                                                                                                   C;Superfamily: transcription initiation factor signa K; transcription initiation fact C;Keywords: DNA binding; sigma factor; transcription initiation factors;Keywords: DNA binding; sigma factor; transcription initiation factor sigma katF homology <KTF>
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A;Molecule type: DNA
A;Residues: 1-213 <COUD
A;Cross-references: EMBL:AF075598; NID:g3293581; PID:g3377838
A;Experimental source: cultivar Columbia
Search completed: June 17,
                                                                                                                                                                                                                                                                                                                                                                        C; Genetics:
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A; Introns: 48/1; 102/3
A; Note: T24H24.20
                                                                                                                                            Query Match 65.4%;
Best Local Similarity 66.7%;
Matches 8; Conservative
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                                                                                                               KLLLKLLLKLL 11
                                                                                    KFLLRLLSKLL
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  2002, 12:42:57
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Pred. No. 1.2e
2; Mismatches
                                                                                                                                                                         Score 34; DB 2; L
Pred. No. 1.3e+02;
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Job time: 252 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein 'protein search, using sw model

Run on: June 17, 2002, 12:39:45 ; Search time 21.35 Seconds (without alignments) 21.763 Million cell updates/sec

Title:
Perfect score:
Sequence: US-09-367-714A-23 52 1 KLLLKLLLKLLK 12

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

15 16 17 18 19 19 19 22 23 24 24 25 27 27 27 27 27 27 27 27 27 27 27 27 27	1 2 2 3 3 4 4 4 5 5 5 6 6 7 7 111 111 111 111 111 111 111 111	Result
3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3		Score
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Query Match 71.2%; Score 37; DB 1; Length 238; Best Local Similarity 80.0%; Pred. No. 15; Matches 8; Conservative 2; Mismatches 0; Indels

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ALIGNMENTS

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EMBL; AE001188; AAC65030.1; TIGR; TP0035; InterPro; IPR003439; ABC_transportr. InterPro; IPR001687; ATP_GTP_A. Pfam: PF00005; ABC_tran; 1. Pfam: PF000051; ABC_TRANSPORTER; FALSE_NEG. PROSITE; PS00211; ABC_TRANSPORT; Inner membrane; ATP-binding; Complete proteome. NP_BIND 44 51 ATP (POTENTIAL). NP_BIND 44 51 ATP (POTENTIAL). SEQUENCE 238 AA; 26460 MW; 673E7B4882BE4D29 CRC64;	YOREPA YORS TREPA YORS TREPA YORS TREPA OBSOTE 16-OCT-2001 (Rel. 40, Last s 17-POOSS Treponema pallidum Bacteria; Spirochaetales; Sp 12-INE-98332770; pubMed=966 MEDLINE-98332770; pubMed=96	LT 1

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P15714;
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01-APR-1990
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Ko C., Smith C.K.
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NCBI_TaxID=5802;
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01-APR-1990 (Rel. 14, Last sequence up
01-FEB-1994 (Rel. 28, Last annotation
Antigen LPMC-61 (Fragment).
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DEVELOPMENTAL STAGE: PRESENT IN ALL STAGES THROUGHOUT THE SPORULATION OF THE OOCYSTS AND IN THE SPOROZOITES FOLLOWING
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3 LVKLVLKLLK 62
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II, McDonell M.;
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81.8%;
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CYCLE, MAY BE AN
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""+ches 7; Conserv?
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                                                      Yasunaga S., Grati M., Chardenoux S., Smith T.N. Lalwani A.K., Wilcox E.R., Petit C.; *OTOF encodes multiple long and short isoforms: the long ones underlie recessive deafness DFNB9. Am. J. Hum. Genet. 67:591-600(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Y00526; CAA68584.1; -. EMBL; Z9911; CAB13238.1; -. PIR; S03747; S03747; S03747; SUBTLIATE BG10770; eag. Hypothetical protein; Sporulatic SEQUENCE 143 AA; 16429 MW; I
MEDLINE=99206603; PubMed=10192385;
                        TISSUE-Fetal
                                   SEQUENCE FROM N.A.
                                                                                                                                             MEDLINE=20395831; PubMed=10903124;
                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                    OTOF_HUMAN STANDARD;
09HC10; 09HC09; 09Y550; 09HC08;
01-MAR-2002 (Rel. 41 Created)
01-MAR-2002 (Rel. 41 Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
0toferlin (Fer-1 like protein 2).
                                                                                                                                                                        TISSUE-Brain
                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                 Homo sapiens (Human).
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01-JAN-1988 (Rel. UV
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16-OCT-2001 (Rel. 4
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5429 MW; D7410B50963D7A75 CRC64;
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protein in SPOOE 3'region.
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us group; Bacillus.
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Catarrhini; Hominidae;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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the European Bioinformatics Institute. The
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Nat. Genet.
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-I- FUNCTION: Might be involved in the Ca(2+)-triggered
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM; 601071;
                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sunaga S., Grati M., Cohen-Salmon M., El-Amraoui A.,
lem N., El-Zir E., Loiselet J., Petit C.;
mutation in OTOF, encoding otoFerlin, a FER-1-like p
NB9, a nonsyndromic form of deafness.";
                                N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE FERLIN SIMILARITY: CONTAINS 4 C2 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE SPECIFICITY: Isoform 1 and isoform 3 are brain. Isoform 2 is expressed in the fetus and heart, placenta, skeletal muscle and kidney. DISEASE: Defects in OTOF are the cause of nonsy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Type II membrane protein (By ALTERNATIVE PRODUCTS: at least 4 isoforms; 1/long 2/short-1, 3/short-2 and 4/short-3; are produced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vesicle-plasma membrane fusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           recessive deafness 9 (DFNB9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF183185; /
AF183186; /
AF183187; /
AF107403; /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is
LLLKLLLLLLL
                              LLLKLLLKLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P04410; 1A25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SM00239;
                                                                Similarity
9; Conserv
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1985
241
404
947
1479
1303
1303
1314
                                                                                                                                                     1088
1997
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                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG12991.1; -.; AAG12992.1; -.; AAG17468.1; -.; AAD26117.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Repeat;
                                11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C2; 6.
1974
                                                                                                                                                     1088
AA; 226735
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1747
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690
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                                                                                 67.3%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OMAIN_1; 2.
OMAIN_2; 4.
Alternative splicing;
                                                                                                                                                                                                               POTENTIAL:

EXTRACELULIAR (POTENTIAL):

C2 DOMAIN 1:

C2 DOMAIN 2:

C2 DOMAIN 3:

C2 DOMAIN 3:

C2 DOMAIN 4.

POLY-LYS:

POLY-LEU:

MISSING (IN ISOFORM 2 AND ISOFORM 4):

MISSING (IN ISOFORM 3):

MISSING (IN ISOFORM 4):

                                                               Score 35; DB
Pred. No. 2.4e
0; Mismatches
                                                               0;
                                                                                                                                                     MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                      IIKIVLALLGLLMLGLFLYSLPGYMVKKLLGA
                                                                                                                                                                                      ISOFORM
                                                                                                                                                                     'n
                                                                                                                                                   L (IN REF. 1; AAG12991)
39D10CB5220638AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FAMILY.
                                                                               DB 1;
2.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Deafness.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Usage
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                                                                                               Length 1997
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(shown here)
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01-OCT-1994
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-95050216; PubMed-7961408;
Sauer U., Treuner A., Buchholz M., Santangelo J.L
"Sporulation and primary sigma factor homologous acetobutylicum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN—ATCC 824 / DSM 792 / VKM B-1787;
MEDLINB-2135925; PubMed-11466286;
Noelling J., Breton G., Omelhenko M.V., Makarova K.S., Zeng
Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., D
Bennett G.N., Koonin E.V., Smith D.R.;
"Genome sequence and comparative analysis of the solvent-pro
bacterium Clostridium acetobitylicum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Bacteriol. 176:6572-6582(1994).

-i- FUNCTION: THE SIGMA FACTOR IS AN INITIATION FACTOR THAT PROMOTES ANTACHMENT OF THE RNA POLYMERASE TO SPECIFIC INITIATION SITES AND THEN IS RELEASED. THIS SIGMA FACTOR IS RESPONSIBLE FOR THE EXPRESSION OF SPORULATION SPECIFIC GENES (BY SIMILARITY).

-i- SIMILARITY: BELONGS TO THE SIGMA-70 FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-ATCC 824 / DSM 792 / VKM B-1787;
Santangelo J.D., Kuhn A., Treuner A., Durre P.;
"Sporulation and time course expression of sigma factor
genes in Clostridium acetobutylicum.";
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE=95189110; PubMed=7883192;
Wong J., Sass C., Bennett G.N.;
"Sequence and arrangement of genes encoding
Clostridium acetobutylicum ATCC 824.";
                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 46-235 FROM N.A. STRAIN-ATCC 824 / DSM 792 / MEDLINE-95050216; PubMed-796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-ATCC 824 / DSM 792
                                                                                                                                                                                                                 EMBL; U07420; AAC43309.1; -. EMBL; Z23079; CAA80617.1; -. EMBL; AE007679; AAK79661.1;
                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clostridium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGE OR CAC1695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteriol. 183:4823-4838(2001).
                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153:89-92(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M., Santangelo J.D., Durre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
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                                                                                                                                                                                                                                                                                                                                                       (See http://www.isb-sib.ch/announce/
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factor; DNA-directed

RNA

polymerase;

PIR; \$34309; \$34309. HSSP; P00579; 1SIG.

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RESULT OF XTMB_BACSU ID WIND_BACSU ID WIND_B
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01-FEB-1995 (Rel. 31, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
PBSX phage terminase large subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-94364963; PubMed-8083174;
McDonnell G.E., Wood H., Devine K.M., McConnell D.J.;
McDonnell G.E., Wood H., McConnell D.J.;
McDonnell G.E., Wood H., McConnell D.J.;
McDonnell G.E., Wood H., McConnell D.J.;
McDonnell D.J.;
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DNA_BIND
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; 270177; CAA94059.1; --
EMBL; 234287; CAA84048.1; --
EMBL; 294110; CAB13115.1; --
PIR; 847115; S47115.
Subtilist; BG11000; xtmB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-76 FROM N.A. STRAIN=168 / SOll3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Krogh S., O'Reilly M., I
Submitted (MAR-1996) to
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NCBI_TaxID=1423;
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2 KFLLRLLSKLL 12
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202
147
235 AA;
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AA; 51150 MW; 471FC77DFEA2CA10 CRC64;
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221 I
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26969 MW;
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o the E
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EMBL/GenBank/DDBJ
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Pred. No.
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H-T-H MOTIF (BY SIMILARITY).
L -> P (IN REF. 4).
; C726E18E6C93A903 CRC64;
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DPOL_NPVBM S
P41712; 092430;
01-NOV-1995 (Rel
15-DEC-1998 (Rel
15-DEC-1998 (Rel
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01-NOV-1990
01-NOV-1995
15-DEC-1998
                                                                                                                                                                                                                                                                            Transferase; DNA-directed DNA polymerase; DNA-binding; Early protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1990 (Rel. 16, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation updat
DNA polymerase (EC 2.7.7.7).
                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                        Pfam; PF00136; DNA_pol_B; 1.
Pfam; PF03104; DNA_pol_B_exo; 1.
PRINTS; PR00106; DNAPOLB.
                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M20744; AAA46692.1; -. EMBL; L22858; AAA66695.1; -. PIR; A31832; DJNVCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=94303173; PubMed=8030224;
Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., I
"The complete DNA sequence of Autographa californica
polyhedrosis virus.";
Virology 202:586-605(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-89073763; PubMed-3059678; Tomalski M.D., Wu J.G., Miller L.K.; "The location, sequence, transcription, baculovirus DNA polymerase gene."; Virology 167:591-600(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DPOL_NPVAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleopolyhedrovirus.
NCBI_TaxID=46015;
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                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002064; DNA_pol_B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    + {DNA}(N).
-!- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY.
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                                                                                                                                             2 LLLKLLLKLL 11
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(Rel. 32, Created)
(Rel. 37, Last sequence up)
(Rel. 37, Last annotation)
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830
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114307
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70.08;
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R -> W (IN REF. 1).

MW; 156ABB6BA1B45A21
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Pred. No. 1.8e+02;
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stage; Baculoviridae;
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a nuclear
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polymerase

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RESULT 9
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Matches 7
                01-NOV-1997
01-NOV-1997
30-MAY-2000
                                             LPL_BUCRP
Q53017;
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Pfam; PF00136; DNA_pol_B; 1.
Pfam; PF03104; DNA_pol_B_exo; 1.
                                                                                                                                                                                                                                                                                                                                                                                             modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bombyx mori nuclear polyhedrosis virus (BmNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                     Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                            use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Sequence analysis of the genome of nucleopolyhedrovirus."; Submitted (OCT-1998) to the EMBL/Ger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chaeychomsri S., Ikeda M., Kobayashi M.;
"Nucleotide sequence and transcriptional
polymerase gene of Bombyx mori nuclear po
Virology 206:435-447(1995).
                                                                                                                                                                                                                                                                                          DNA-binding;
                                                                                                                                                                                                                                                                                                                       PRINTS; PR00106; DNAPOLB. SMART; SM00486; POLBC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute.
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LEUL OR LEUO.
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SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY
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                                                                                                                     LLLKLLKLL
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                                                                                                                                        Similarity 7; Conserv
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                                                                                                                                                                                                                                                                                                              DNA_POLYMERASE_B;
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39,
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70.0%;
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                                     Created)
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N deoxynucleoside triphosphate =
                          sequence update)
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S -> G (I
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Pred. No.
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POLY-ASP.
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A -> S (I
H -> Y (I
H -> Y (I
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                                                                                                                                       1.8e+02;
ches 0;
                                                                                                                                                                                                (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           al analysis of the DNA polyhedrosis virus.";
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                                                                                           C STRAIN-ATCC 27343;

X MEDLINE-94051609; PubMed-8233831;

A Miyata M., Sano K.-I., Okada R., Fukumura T.;

A Miyata M., Sano K.-I., Okada R., Fukumura T.;

A Miyata M., Sano K.-I., Okada R., Fukumura T.;

A Miyata M., Sano K.-I., Okada R., Fukumura T.;

A Miyata M., Sano K.-I., Okada R., Fukumura T.;

A Miyata M., Sano K.-I., Okada R., Fukumura T.;

B "Mapping of replication initiation site in Mycoplasma capricolum T genome by two-dimensional gel-electrophoretic analysis.";

I Nucleic Acids Res. 21:4816-4823(193).

C -!- FUNCTION: Rassep catalyzes the removal of the 5'-leader sequence the mature 5'terminus. It can also cleave other RNA substrates such as 4.5S RNA. The protein component plays an auxiliary but essential role in vivo by bindi to the 5'-leader sequence and broadening the substrate specificity of the ribozyme (By similarity).

C -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage of RNA, removing 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local
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P43039;
01-NOV-1995
01-NOV-1995
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95333198; PubMed=7608990; MEDLINE=95333198; PubMed=7608990; Bracho A.M., Martinez-Torres D., Moya A., Latorre A.; "Discovery and molecular characterization of a plasmid localized Buchnera sp. bacterial endosymbiont of the aphid Rhopalosiphum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leader peptide; SEQUENCE 31 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Bacteria; Firmicutes;
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Plasmid pRPE.
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=2095
                                                                                                                                                                                                                                                                                                                                 Entomoplasmataceae
                                                                                                                                                                                                                                                                                                                                                                             RNPA.
                                                                                                                                                                                                                                                                                                                                                                                         (RNase P protein) (Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KLLLKLLLKLL
                                       protein subunit (By similarity).
SIMILARITY: BELONGS TO THE RNPA FAMILY
                                                                    extra-nucleotide from tRNA precursor. SUBUNIT: Consists of a catalytic RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OF LEUCINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KLLLLLLLYLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Evol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proteobacteria; gamma subdivision; Buchnera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41:67-73(1995).
THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leucine
A; 3920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63
81
                                                                                                                                                                                                                                                                                                                                               Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . 5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MW; 4D3E5E1C31C85413
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Pred.
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No.
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3.1.26.5)
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11;
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                                                                    component
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                          (RNaseP protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 31;
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This SWISS-PROT entry is copyright. between the Swiss Institute of Bio

Bioinformatics

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EMBL

outstation

a collaboration

g 200

97

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11

Matches

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DCAM_RAT
P17708;
01-AUG-1990
01-JUL-1993
16-OCT-2001
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SEQUENCE FROM N.A.
MEDLINE=90215298; PubMed=2323572;
MEDLINE=90215298; PubMed=2323572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-92038024; PubMed=1936275;
MEDLINE-92038024; PubMed=1936275;
Pulkka A., Ihalainen R., Aatsinki J., Pa
"Structure and organization of the gene
adenosylmethionine decarboxylase.";
FEBS Lett. 291:289-295(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1990 (Rel. 15, Created)
01-JUL-1993 (Rel. 25, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
5-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50) (SamDC) [Contains: S-adenosylmethionine decarboxylastationine decarboxylase alpha adenosylmethionine decarboxylase beta chain].
                  S-adenosylmethionine decar
Genomics 16:342-349(1993).
-!- CATALYTIC ACTIVITY: S-
                                                                                                  SEQUENCE FROM N.A.
STRAIN-WISTAR: TISSUE-Spleen;
MEDLINE-93300506; PubMed-8314573;
Pulkka A., Thalainen R., Suorsa A
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-89034205; PubMed~2460457;
PaiJunen A., Crozat A., Jaenne O.A., Ihalainen R., Laitinen P.H.,
Stanley B., Madhubala R., Pegg A.E.;
"Structure and regulation of mammalian S-adenosylmethionine"
                                                                 Pajunen A.; "Structures and chromosomal localizations of two
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Comparison with an int
Gene 86:193-199(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000100; Ribonuclease_P.
Pfam; PF00825; Ribonuclease_P: 1.
PROSITE; PS00648; RIBONUCLEASE_P: 1.
Hydrolase; Nuclease; Endonuclease; tRNA processing; RNA-binding.
SEQUENCE 109 AA; 12900 MW; ACF520A0982CDD12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D14982; BAA03619.1; HSSP; P25814; 1A6F.
                                                                                                                                                                                                                                                                                                                                 decarboxylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleotide sequence of rat S-adenosylmethionine comparison with an intronless rat pseudogene.";
  CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (5-deoxy-5 adenosyl)(3-aminopropyl) methylsulfonium salt + CO(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LSKLLIKLIK 106
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7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                263:17040-17049(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                   decarboxylase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; |
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                      A., Riviere M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Α.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     333
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                                                                                                      Szpirer
                                                                                                                                                                                                                             rat
                                                                   rat genes encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        decarboxylase cDNA
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; Murinae; Rattus
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a chain; S-
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DCAM_BOVIN

DCAM_B
AC P5024,B
AC P5024,B
AC P5024
DT 01-0CT
DT 16-0CT
DT 16-0CT
DE S-aden
DE (Samp)
DE adenoe
GN ABD1
OC BOV1dd
OC MCBL_1
RN [1]
RP SEQUEI
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Best Local
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EMBL; M64274; AAA42105.1;
EMBL; 215109; CAA78814.1; J
EMBL; Z15122; CAA78814.1; J
EMBL; Z15123; CAA78814.1; J
EMBL; Z15123; CAA78814.1; J
PIR; J00439; DCRTDM.
PIR; S10487; S18487.
                Bos taurus (Bovine).
Eukaryota; Metazoa; C
Mammalia; Eutherla; C
Bovidae; Bovinae; Bos
NCBI_TaxID-9913;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                DCAM_BOVIN STANDARD; PRT; 334 AA.
P50243;
P50243;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50)
(SamDC) [Contains: S-adenosylmethionine decarboxylase alpha adenosylmethionine decarboxylase beta chain].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOD_RES
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P17707; 1JEN.
InterPro; IPR001985; SAM_decarbox.
Pfam; PF01536; SAM_decarbox; 1.
Probom; PD002379; SAM_decarbox; 1.
PROSITE; PS01336; ADOMETDC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY) BELONGS TO THE BUKARYOTIC ADONETIC FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---
  SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                 86 LLLKALVPLLK
                                                                                                                                                                                                                                                                                                                                                                              2 LLLKLLKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COFACTOR: PYRUVOYL GROUP.

PATHHAY: DECARBOXYLAFION OF S-ADENOSYLMETHIONINE PROVIDES THE AMINOPROPYL MOIETY REQUIRED FOR SPERMIDINE AND SPERMINE BIOSYNTHESIS FROM PUTRESCINE.

SUBUNIT: HETEROTETRAMER OF TWO ALPHA AND TWO BETA CHAINS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 72. 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146
333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82
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68
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146
38137 .
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                                                   Bos.
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                                                                 Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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6 9 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                 72.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18; Lyase; Decarboxylase; Pyruvate; Zymogen, S-ADEMOSYLMETHIONINE DECARBOXYLASE BE CHAIN.

3 S-ADEMOSYLMETHIONINE DECARBOXYLASE AL CHAIN.

3 CLEAVAGE (NONHYDROLYTIC):

4 CLEAVAGE (NONHYDROLYTIC):

5 CONVERTED TO A PYRUVOYL GROUP.

5 IMPLANTY);

6 SIMILARITY);

6 LIMPORTANT FOR CATALYTIC ACTIVITY (BY SIMILARITY);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOINED
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                                                                                                                                                                                                                                                                                                                                                                                                                 Score 33; DB Pred. No. 98; 1; Mismatches
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A -> G (IN REF. 1).
; 9323E2D38BD8FEF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY).
IMPORTANT FOR CATALYTIC SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 333;
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PRESULT 1
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DCAM_RAT 1
DCAM_RAT 1
DCAM_RAT 1
DCAM_RAT 1
DT 01.-C.
D

(AdoMetDC) a chain; S-

0;

Gaps

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RESULT 13
DCAM_HUMAN
ID DCAM_H
AC P17707
DT 01-AUG
DT 01-AUG
DT 16-OCT
DE S-aden
DE (SamD)
DE (SamD)
OS HOMO S
OS HOMO S
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Best Local
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                                                                DCAM_HUMAN STANDARD; PRT; 334 AA.

P17707; Q9BWK4;

01-AUG-1990 (Rel. 15, Created)

01-AUG-1990 (Rel. 15, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

5-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50) (AdoMetDC)

(SamDC) [Contains: S-adenosylmethionine decarboxylase alpha chain; S-ad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hill J.R.,
Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF01536; SAM_decarbox; 1.
ProDom; PD002379; SAM_decarbox; 1.
PROSITE; PS01336; ADOMETDC; 1.
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   adenosyl)(3-aminopropyl) methylsulfonium salt
-:- COFACTOR: PYRUVOYL GROUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mach M., White M.W., Neubauer M., De
"Isolation of a cDNA clone encoding
decarboxylase. Expression of the ge
                                                              adenosylmethionine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities
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                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACT_SITE
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                                                                                                                                                                                                                                                                                                        86 LLLKALVPLLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE EUKARYOTIC ADOMETDC FAMILY.
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Pro; IPR001985; SAM_decarbox.
                                                                                                                                                                                                                                                                                                                                                                               h 63.5%;
Similarity 72.7%;
8; Conservative
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and this statement is not removed. Usage by ar
requires a license agreement (See http://www.isb
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  Metazoa; Chordata;
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CONVERTED TO A PYRUVOYL C
IMPORTANT FOR CATALYTIC F
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  Craniata;
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                                                            beta
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in mitogen-act'
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(See http://www.isb-sib.ch/announce/
                                                            chain]
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  Vertebrata; Euteleostomi;
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MOD_RES
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                                  ACT_SITE
                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDILINE-92011599; PubMed-1917972;
Stanley B.A., Pegg A.E.;
"Amino acid residues necessary for putrescine stimulation of human s
                                                                                                                                              SITE
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between the Swiss Institute of Bioinformatics and the EMBL
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Ekstrom J.L., Mathews I.I., Stanley B.A., Pegg A.E.,
"The crystal structure of human S-adenosylmethionine
2.25-A resolution reveals a novel fold.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       activity.
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MEDLINE-89034205; PubMed-2460457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria;
NCBI_TaxID=9606;
   MUTAGEN
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the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                      Pfam; PF01536; SAM_decarbox;
                                                                                                                                                                                                                                                                                                                                       MIM; 180980;
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                                                                                                                                                                                                                               3D-structure.
                                                                                                                                                                                                                                                   Spermidine biosynthesis;
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                                                                                                                                                                                                                                                                                                                       InterPro; IPR001985;
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SIMILARITY:
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PATHWAY: DECARBOXYLATION OF S-ADENOSYLMETHIONINE PROVIDES
AMINOPROPYL MOIETY REQUIRED FOR SPERMIDINE AND SPERMINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BIOSYNTHESIS FROM PUTRESCINE.
                                                                                                                                                                                                                                                                                                                                                        1JEN; 01-JUN-99.
                                                                                                                                                                                                                                                                                                                                                                                       M21154; AAA51716.1; -. BC000171; AAH00171.1;
                                                                                                                                                                                                                                                                                                                                                                                                           M21154; AAA51716.1;
                                                                                                                                                                                                                                                       PD002379; SAM_decarbox; 1. PS01336; ADOMETDC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                          non-profit institutions as long d and this statement is not removed. s requires a license agreement (See an email to license@isb-sib.ch).
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68
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of mammalian
CLEAVAGE (NONHYDROLYTIC).

CONVERTED TO A PYROVOYL GROUP.

IMPORTANT FOR CATALYTIC ACTIVITY.

IMPORTANT FOR CATALYTIC ACTIVITY, AND
PUTRESCINE STIMULAION OF PROCESSING.

IMPORTANT FOR CATALYTIC ACTIVITY.

E-Q: LOSS OF ACTIVITY. NORMALL

PUTRESCINE-STIMULATED PROCESSING.

E-Q: LOSS OF ACTIVITY. LOSS OF
                                                                                                                                                             S-ADENOSYLMETHIONINE DECARBOXYLASE ALPHA CHAIN.
                                                                                                                                                                                                                S-ADENOSYLMETHIONINE
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                                                                                                                                                                                                                                                 Pyruvate;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (5-deoxy-5-
+ CO(2).
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decarboxylase
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RESULT 14
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Best Local s
Matches 8
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01-DEC-1992
16-OCT-2001
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MUTAGEN
MUTAGEN
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochim. Biophys. Acta 1130:221-223(1992).

-!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (5-deoxy-5-adenosyl)(3-aminopropyl) methylsulfonium salt + CO(2).
-!- COEACTOR: PYRUPYL GROUP.
-!- PATHWAY: DECARBOXYLATION OF S-ADENOSYIMETHIONINE DECAYBOXYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=92223099; PubMed=1562599;
Tekwani B.L., Stanley B.A., Pegg A.E.;
"Nucleotide sequence of hamster S-adenosylmethionine decarboxylase
cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
5-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50) (SamDC) [Contains: S-adenosylmethionine decarboxylase alpha adenosylmethionine decarboxylase alpha adenosylmethionine decarboxylase beta chain).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MUTAGEN
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Eukaryota; Metazoa; Chordata; Craniata.
Mammalia; Eutheria; Rodentia; Sciurogna
                                                                                                                                                                           EMBL;
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SUBUNIT: HETEROTETRAMER OF TWO ALPHA AND TWO BETA CHAINS (BY
                                            X63861; CAA45343.1;
S19871; DCHYDM.
S22358; S22358.
; P17707; LJEN.
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    IPR001985;
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E-9Q: LITTLE EFFECT.
C-9A: LITTLE EFFECT.
E-9Q: LITTLE EFFECT.
E-9Q: LITTLE EFFECT.
K-9A: GREATLY REDUCED CATALYTIC ACTIVITY. NO PUTRESCINE-STIMULATED PROCESSING.
C-9A: LOSS OF ACTIVITY. GREATLY REDUCED PROCESSING.
C-9A: LOSS OF ACTIVITY. GREATLY REDUCED FROCESSING.
C-9A: LOTTLE EFFECT.
E-9Q: LITTLE EFFECT.
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Sciurognathi; Muridae; Cricetinae;
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LOUISE

DCMI_MOUSE STANDARD; PRT; 334 AA.

P31154;
01-UTL-1993 (Rel. 26, Created)
01-UTL-1993 (Rel. 26, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
5-adenosylmethionine decarboxylase proenzyme 1 (EC 4.1.1.50)
1 (Samd 1) [Contains: S-adenosylmethionine decarboxylase 1 beta chain].
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PrODom; PD002379;
PROSITE; PS01336; J
Spermidine biosyntl
CHAIN
STRAIN-129/SVJ; TISSUE-Spleen;
MEDLINE-20035739; PubMed-10570962;
MEDLINE-20035739; PubMed-10570962;
Nishimura K., Kashiwagi K., Matsuda Y., Jaenne O.A., Igarashi igene structure and chromosomal localization of mouse s-adenosylmethionine decarboxylase.";
Gene 238:343-350(1999).
-!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (5-deoxy-5-adenosyl)(3-aminopropyl) methylsulfonium salt + CO(2).
-!- COFACTOR: PYRUYOYL GROUP.
-!- PATHWAY: DECARBOXYLATION OF S-ADENOSYLMETHIONINE PROVIDES:
AMINOPROPYL MOIETY REQUIRED FOR SPERMIDINE AND SPERMINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOD_RES
                                                                                                                                                                                                                                                            MEDILINE-93345510; PubMed=8344293;
Suzuki T., Sadakata Y., Kashiwagi K., Hoshino K., Kakinuma Y., Shirahata A., Igarashi K.;
"Overproduction of S-adenosylmethionine decarboxylase in ethylglyoxal-bis(guanylhydrazone)-resistant mouse FM3A cells.";
Eur. J. Biochem. 215:247-253(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                          Waris T., Ihalainen R., Keraenen M.-R., Pajunen A.; "Molecular cloning of the mouse S-adenosylmethionine decarboxylase CDNA: specific protein binding to the conserved region of the mRNA 5/-untranslated region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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MEDLINE=93345510;
                                                                                                                                                                                                                                                                                                                                                                                                                        Biochem. Biophys. Res. Commun. 189:424-429(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-C57BL/6; TISSUE-Brain;
MEDLINE-93080592; PubMed=1449493;
Waris T., Ihalainen R., Keraenen
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                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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79; SAM_decarbox; 1.
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72.7%;
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S-ADENOSYLMETHIONINE DECARBOXYLASE BETA
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CLEAVAGE (NONHYDROLYTIC).
CONVERTED TO A PYRUVOYL GROUP.
IMPORTANT FOR CATALYTIC ACTIVITY
SIMILARITY).
IMPORTANT FOR CATALYTIC ACTIVITY
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Pred. No.
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S-ADENOSYLMETHIONINE DECARBOXYLASE ALPHA
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IMPORTANT FOR CATALYTIC
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Search completed: June 17, 2002, 12:44:45 Job time: 300 sec
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Best Local Similarity
Matches 8; Conserv
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MOD_RES
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z14986; CAA78710.1; -. EMBL; D12780; BAA02243.1; -. EMBL; AB025024; BAA83784.1; -. HSSP; P17707; 1JEN.
                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pram; PF01536; SAM_decarbox; 1. ProDom; PD002379; SAM_decarbox; 1. PROSITE; PS01336; ADOMETDC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:88004; Amd1:
InterPro; IPR001985; SAM_decarbox.
Pfam; PF01536; SAM_decarbox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BIOSYNTHESIS FROM PUTRESCINE.
-!- SUBUNIT: HETEROTETRAMER OF TWO ALPHA AND TWO BETA CHAINS SIMILARITY).
-!- SIMILARITY: BELONGS TO THE EUKARYOTIC ADOMETDC FAMILY.
                                                                                                                                                                                                                                                                                                  ACT_SITE
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                                                                                               86 LLLKALVPLLK 96
                                                                                                                  2 LLLKLLLKLLK 12
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                                                                                                                                                                                                                                                                334 AA;
                                                                                                                                                                    Conservative
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68
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72.7%;
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                                                                                                                                                                                     Score 33;
Pred. No.
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CONVERTED TO A PYRUVOYL GROUP.
IMPORTANT FOR CATALYTIC ACTIVITY
                                                                                                                                                                                                                                                        SIMILARITY).
; 7950A1E9A9ACBD72 CRC64;
                                                                                                                                                                                                                                                                                       SIMILARITY).
IMPORTANT FOR CATALYTIC ACTIVITY (BY
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IMPORTANT FOR CATALYTIC ACTIVITY (BY
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S-ADENOSYLMETHIONINE DECARBOXYLASE 1
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Mismatches
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Q9PI84
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O9bc70 sargassum p
Q941q5 oryva sativ
O961k7 homo sapien
Q95xu2 caenorhabdi
Q95yh3 schizophyll
O64604 arabidopsis
O9cp24 pasteurella
Q9p184 campylobact
O51049 borrelia bu
Q9y650 homo sapien
Q9hc10 homo sapien
Q9hc10 homo sapien
Q9hc10 homo sapien
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Q91pm4 arabidopsis
Q97ms6 clostridium
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staphyloco		Q97s99 streptococc	Q950q3 spizellomyc	Q9g905 ochromonas		Q932m8 staphylococ	\vdash	051404 borrelia bu		Q99yw0 streptococc	Q91fk0 chilo iride	Q9nef9 drosophila					æ	streptoc	O58557 pyrococcus	Q973p4 sulfolobus		Q9zlz4 helicobacte		Q9ac69 staphylococ	sulfol	5 chilo	O55758 chilo iride	aphidi

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Pfam; PF02250; FAT; 1.

Pfam; PF00454; PI3_PI4_kinase; 1.

SMART; SM00146; PI3KC; 1.

SMART; SM00146; PI3KC; 1.

PROSITE; PS00915; PI3_4_KINASE_1; 1.

PROSITE; PS50290; PI3_4_KINASE_3; 1.

SEQUENCE 2481 AA; 279187 MW; DA663
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01-MAR-2001
01-DEC-2001
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STRAIN-CV. COLUMBIA;
Menand B., Nussaume L., Meyer C., Desnos T., Bouchez D.,
"Mutation in AtTOR affects embryo development.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AFI18967; AAG43423.1; -.
HSSP; P42345; IFAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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InterPro; IPR003152; FATC.
InterPro; IPR000403; PI3_PI4_kinase.
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(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                              Conservative
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                                                                                                                 76.9%;
90.9%;
                                                                              0;
                                                                                                                 Score 40; DB 10;
Pred. No. 1.7e+02;
                                                                              Mismatches
                                                                                                                                                                                                                                                                      DA663EA9A9366F93 CRC64;
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01-OCT-2000
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01-DEC-2001
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PROSITE;
PROSITE;
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 SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=ATCC 824 / DSM 792 / VKM B-1787;

STRAINE-21359325; PubMed-11466286;

McDlling J., Breton G., Omelchenko M.V.,

Gibson R., Lee H.M., Dubois J., Qiu D., I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                     Clostridium acetobutylicum.
Bacteria; Firmicutes; Bacillus/Clostridium
Clostridium.
CCBI_TaxID=1488;
                                                                                                                                                 097MS6;
01-0CT-2001 (TrEMBLrel. 18, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
UNCHARACTERIZED PROTEIN, YJE/RRF2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=CV.
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; SM00146; PI3Kc; 1.
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SM0015; PI3 4_KINASE_1; 1

SM00915; PI3 4_KINASE_2; 1

SM00916; PI3 4_KINASE_3; 1

SM00916; PI3 4_KINASE_3; 1

E 2513 AA; 282911 MW; A4
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IPR003152; FATC
IPR000403; PI3_
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             Qiu D., Hitti
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1.7e+02;
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  Makarova K.S.,
Hitti J., Wolf !
L., Soucaille !
                                                                                                               group; Clostridiaceae;
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Davis R.W.,
   Daly M.J.,
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RESULT
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EMBL; AE007524; AAK78100.1;
InterPro; IPR000944; UPF0074.
Pfam; PF02082; UPF0074; 1.
ProDom; PD003632; UPF0074; 1.
PROSITE; PS01332; UPF0074; 1.
                                                         Carbon dioxide fixation; Chloroplast; Oxidoreductase; Photorespiration; PhotoRDUENCE 53 AA.
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Q9BC70;
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN (EC 4
LARGE SUBUNIT) (FRACMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete proteome. SEQUENCE 137 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bacterium Clostridium acetobutylicum.
J. Bacteriol 183:4823-4838(2001).
                                                                                                                                                                          -!- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + CO(2) = PHOSPHO-GLYCERATE.
-!- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + O(2) = PHOSPHO-D-GLYCERATE + 2-PHOSPHOGLYCOLATE.
-!- SUBUNIT: 8 LARGE CHAINS + 8 SMALL CHAINS (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bennett
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. Phillips N., Frede
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sargassum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genome to G.N., Koonin E.V., Smith D.R.;
genome sequence and comparative analysis of the solvent-producing
                                                                                                                                   -!- SIMILARITY: BELONGS TO THE RUBISCO EMBL; AF301225; AAK01554.1; -. InterPro; IPR000685; RuBisCO_large.
                                                                                                                                                                                                                                                                                                                                                                      Sargassum
                                                                                                                                                                                                                                                                                                                                                                     Phillips N., Fredericq S.;
"Biogeographic and phylogenetic investigation of the pan-pacific genus
Sargassum (Fucales, Phaeophyceae) with respect to the Gulf of Mexico
                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=143167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40 RFLLKLLRKLIK
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                                                                                                                                                                                                                                                           FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION OF RIBULOSE 1.5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE SITE (BY SIMULTANEOUSLY AND IN COMPETITION AT THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KLLLKLLKLLK
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8; Conserv
Similarity 72...
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polyceratium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      stramenopiles;
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66
               69
72
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               .78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2
  Score 36; DB
Pred. No. 29;
2; Mismatches
  2;
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                                                                    6E4CD0DCA9CE531B
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                                                                                              Photosynthesis
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              DB
29;
                                                                                                                                                                 LARGE CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fucales;
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                                                                                                            Monooxygenase;
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                                                                      CRC64;
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Best Local S
Matches 8
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Best Loc
Matches
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"NEDO human CDNA sequencing project.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q94LQ5;
01-DEC-2001
01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brenner M., Burgess S., Hance M., Shvartsbeyn M., Tsitrii Riggs F., Hsiao J., Zismann V., Blunt S., Pai G., VanAker Utterback T.R., Feldblyum T.V., Quackenbush J., Salzberg White O., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Oryza sativa chromosome 10 Submitted (MAY-2001) to the EMBL; AC069300; AAK55450.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CV. NIPPONBARE;
Buell C.R., Yuan Q., C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa (Rice).
Eukaryota; Viridiplantae;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 8.1 KDA PROTEIN.
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                                                                                                                                                                                                                               SEQUENCE
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  KSLTKYLLKLLK
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9; Conserv
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8; Conser
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nilarity 66.7%;
Conservative
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Primates;
                                                                                                                          69.2%;
75.0%;
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                                                                                                                                                                                                                               MW;
                                                                                             Score 36; DB Pred. No. 1e+0
0; Mismatches
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EMBL/GenBank/DDBJ
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Catarrhini; Hominidae;
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                                                                                                                          DB 4;
1e+02;
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databases.
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                                                                                                                                               Length 237;
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Best Local :
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01-MAR-2001 (TrEMBLIEL. I.
01-MAR-2001 (TrEMBLIEL. II
01-DEC-2001 (TrEMBLIEL. 1
01-DEC-2001 (TREMBLIEL. 1
                                               SEQUENCE FROM N.A. MEDLINE=20377911; Pu Bullerwell C.E., Bus "A novel motif for i
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01-DEC-2001
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01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
HYPOTHETICAL 127.2 KDA P
                                                                                                         Eukaryota; Fungi; Basidiomycota; Hymenomyco
Stereales; Schizophyllaceae; Schizophyllum
NCBI_TaxID-5334;
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982 ILKLLLRLIK
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Submitted (NOV-2001) to the
EMBL; AC024848; AAK68543.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN=BRISTOL N2; Edwards J., Lamar B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              investigating biology. The C. elegans Sequencing Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN=BRISTOL N2; MEDLINE=99069613;
[2]
SEQUENCE FROM
                                    genomes
                                                                                                                                                   Mitochondrion.
                                                                                                                                                               Schizophyllum
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Rhabditidae; Peloderinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   l protein
1107 AA;
                                                                                                                                                                                                                                                                                                                                                                     Conservative
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 N.A.
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                                                Burger G., Lang B.I
or identifying rps3
                                                                       PubMed=10916154;
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O) to the
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                                                                                                                                                                                                                                                                                                                                                                                 69.2%;
70.0%;
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1. 19, Last
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1. PROTEIN.
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Last
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Last annotation updat
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EMBL/GenBank/DDBJ
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Pred. No. 3.
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Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AC003671; AAC18812.1; -.
InterPro; IPR002950; Josephin.
InterPro; IPR000449; UBA.
InterPro; IPR003903; UIM.
Pfam; PF00867; UBB; 1.
Pfam; PF02809; UIM; 1.
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01-AUG-1998 (TREMB
01-BEC-2001 (TREMB
F1707.14 PROTEIN.
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STRAIN-CV. COLUMBIA;
Vysotskaia V.S., Schwartz J.R., Toriumi M., Yu G., Kwan A., Oji
Liu S., Li J., Araujo R., Au M., Brendel V., Buehler E., Conway
Conway A.R., Dewar K., Feng J., Kim C., Kurtz D., Li Y., Palm C.
Shinn P., Sun H., Davis R.W., Ecker J.R., Federspiel N.A.,
Theologis A.;
                                                                                                                                                                                                                                                         Submitted
                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Mitochondrion.
1453 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUL-2001) to the EMBL; AF402141; AAG10295.1;
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Pred. No. 4.9e+02;
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Q9P184;
01-OCT-2000
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SEQUENCE
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STRAIN-NCTC 11168;

MEDLINE-20150912; PubMed-10688204;

MEDLINE-20150912; PubMed-10688204;

Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.

Basham D., Chillingworth T., Davies R.M., Feltwell T., Holro

Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,

Quail M.A., Rajandaream M.A., Rutherford K.M., van Vliet A.H.

Whitehead S., Barrell B.G.;

"The genome sequence of the food-borne pathogen Campylobacte
                                                                                       reveals hypervariable sequences.";
Nature 403:665-668(2000).
EMBL; AL139075; CAB74257.1; -.
                                                                                                                                                                                                                                                            Campylobacter.
NCBI_TaxID=197;
                                                                                                                                                                                                                                                                                   Campylobacter jejuni.
Bacteria; Proteobacteria;
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01-JUN-2001
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MEDLINE=21145866; PubMed=11248100;
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Bacteria; Proteobacteria;
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MEDLINE=98065943; PubMed=9403685;
Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwi
Dougherty B., Tomb J.-F., Fleischnann R.D., Richardson D.,
Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hansor
van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
Utterback T., Watthey C., Cotton M.D., Horst K., Roberts K., Hatch
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01-NOV-1999
01-JUN-2001
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01-JUN-1998
01-JUN-1998
01-JUN-2001
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                                                                                      Yasunaga S., Grati M., Cohen-Salmon M., E Salem N., El-Zir E., Loiselet J., Petit C "A mutation in O'DOF, encoding otoferlin, DFNB9, a nonsyndromic form of deafness.", Dat. Genet. 21:35-369(1999).
EMBL: AFIO7403; AAD26117.1; -.
HSSP; P04410; 1A25.
                     InterPro; IPR000008; C2. Pfam; PF00168; C2; 2. PRINTS; PR00360; C2DOMAI
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MEDLINE=99206603; PubMed=10192385;
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                               Chordata;
Primates;
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C.;
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D.,
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DR
SQ
                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Pr
NCBI_TaxID=9606;
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MEDLINE-20395831; PubMed-10903124;
Yasunaga S., Grati M., Chardenoux S., Smith T.N.
Lalwani A.K., Wilcox E.R., Petit C.;
Lalwani P.K., Wilcox E.R., Petit C.;
"OTOF encodes multiple long and short isoforms:
the long ones underlie recessive deafness DFNB9.
Am. J. Hum. Genet. 67:591-600(2000).
EMBL, AF183186; AAG12992.1; --
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PROSITE;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00499; C2_DOMAIN_1; PROSITE; PS50004; C2_DOMAIN_2; SEQUENCE 1307 AA; 148926 MW;
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Pfam; PF00168; C2; 2.
PRINTS; PR00360; C2DOMAIN.
SMART; SM00239; C2; 3.
Yasunaga S., Grati M., Chardenoux Lalwani A.K., Wilcox E.R., Petit (
                          SEQUENCE FROM N.A. MEDLINE-20395831;
                                                                                                                                   BRAIN OTOFERLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P04410; 1A25.
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Mammalia; Eutheria;
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PS50004; C2_DOMAIN_2;
1230 AA; 140496 MW;
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ERLIN SHORT IS
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(TrEMBLrel. 16, Last sequence update)
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                                                                                                                                                                                                                                                                                                                            Conservative
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Primates;
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Catarrhini;
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Page 6
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RT "OTOF encodes multiple long and short isoforms: genetic evidence that the long ones underlie recessive deafness DFNB9.";

Am. J. Hum. Genet. 67:591-600(2000).

DR EMBL, AF183185; AAG12991.1;

DR HSSP; P04410; IA25.

DR InterPro; IPR000008; C2.

DR Pfam, PF00166; C2; 4.

DR PRINTS; PR00360; C2:DOMAIN.

DR SMART; SM00239; C2; 6.

DR PROSITE; PS0049; C2:DOMAIN.2; 4.

SQ SEQUENCE 1997 AA; 226751 MW; 24DE196371FB7385 CRC64;

Ouery Match
Best Local Similarity 90.0%; Pred. No. 9.5e+02;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 1965 LLIKILLEL 11

Db 1965 LLIKILLEL 1974

Search completed: June 17, 2002, 12:44:18

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OM protein - protein search, using sw model
June 17, 2002, 12:38:20 ; Search time 34.71 Seconds (without alignments) 8.444 Million cell updates/sec
                                                                                                                                                                                                            GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Title: Perfect score: Sequence: US-09-367-714A-23 52

Scoring table: 1 KLLLKLLKLLK 12

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters:

231628 seqs, 24425594 residues

231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2,
2: //gn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: //gn2_6/ptodata/2,
5: //gn2_6/ptodata/2,
6: //gn2_6/ptodata/2, /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	თ	U	4	ω	N	1	Result No.
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Query Match 76.9%; Score 40; DB 2; Best Local Similarity 83.3%; Pred. No. 1.5; Matches 10; Conservative 0; Mismatches

2; Indels Length 14;

0; Gaps

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4 5	44	43	42	41	40	39	38	37	36	35	34	33	32	3 <u>1</u>	30	29	28
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67.3	71.2	71.2	71.2	71.2	71.2	71.2	71.2	71.2	71.2	71.2	71.2	71.2	71.2	71.2	71.2	71.2	71.2
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US-07-725-331-4	PCT-US94-07019-15	PCT-US94-07019-6	US-09-296-089-36	US-08-958-993A-12	US-08-960-054A-12	US-08-569-188-15	US-08-569-188-6	PCT-US94-07019-14	PCT-US94-07019-4	US-08-569-188-14	US-08-569-188-4	PCT-US94-07019-13	PCT-US94-07019-2	US-08-569-188-13	US-08-569-188-2	PCT-US91-05047-1	US-07-725-331-1
Sequence 4, Appli	Sequence 15, Appl	Sequence 6, Appli	•	-	Sequence 12, Appl		Sequence 6, Appli	Sequence 14, Appl	Sequence 4, Appli	Sequence 14, Appl	Sequence 4, Appli	Sequence 13, Appl	Sequence 2, Appli	Sequence 13, Appl	Sequence 2, Appli	Sequence 1, Appli	Sequence 1, Appli

ALIGNMENTS

Patent No. 5847047 GENERAL INFORMATION: APPLICANT: SHARON LPRETTA HAYNIE TITLE OF INVENTION: NOVEL ANTIMICORBIAL COMPOSITIONS NUMBER OF SEQUENCES: 18 CORRESSOES: 1. DU PONT DE NEMOURS AND COMPANY STREET: 1007 MARKET STREET COUNTRY: WILMINGTON STATE: DELAWARE COUNTRY: WILMINGTON STATE: DELAWARE COMPUTER READABLE FORM: MEDIIN TYPE: DISKETTE, 3.50 INCH COMPUTER READABLE FORM: MEDIIN TYPE: DISKETTE, 3.50 INCH COMPUTER NICROSOFT WORD FOR WINDOWS 95 SOFTWARE: MICROSOFT WORD FOR WINDOWS 95 SOFTWARE: MICROSOFT WORD FOR WINDOWS 95 CLASSIFICATION NUMBER: US/08/569,188 FILING DATE: APPLICATION NUMBER: US/08/569,188 FILING DATE: CLASSIFICATION NUMBER: US/08/569,188 FILING DATE: JUNE 22, 1993 ATTORNEY/AGENT INFORMATION: APPLICATION NUMBER: 33,692 REFERENCE/DOCKET NUMBER: CR-9295-A TELECOMMUNICATION NUMBER: GR-9295-A TELECOMMUNICATION NUMBER: US/08/569,188	RESULT 1 US-08-569-188-8
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PCT-US94-07019-8

Sequence 8, Application PC/TUS9407019 GENERAL INFORMATION:

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KKLLKLLKKLLK 13

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APPLICATION NUMBER: 08/082,8:
FILING DATE: JUNE 22, 1993
INFORMATION FOR SEO ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acids
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
PCT-US94-07019-8
                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-569-188-1
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08569188 Patent No. 5847047
 NAME: LINDA AXAMETHY FLOYD REGISTRATION NUMBER: 33,692 REFERENCE/DOCKET NUMBER: CR-9295-A TELECOMMUNICATION INFORMATION:
                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/0
FILING DATE: JUNE 22, 19
ATTORNEY/AGENT INFORMATION,
NAME: LINDA AXAMETHY FILE
                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                 MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD FOR WINDOWS 95 (7.0)
APPLICATION NUMBER: US/08/569,188
FILING DATE:
                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTI
                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: SHARON I
                                                                                                                                                                                                                                                  COUNTRY: UM
                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                         CLASSIFICATION:
                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT AT LON NUMBER: PCT/USST/ LAPPLICATION NUMBER: PCT/USST/ LAPPLICATION NUMBER: 08/082,852
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                               WILMINGTON
                                                                                                                                                                                                                                                                                 DELAWARE
                                                                                                                                                                                                                                                                                               E: E. I. DU PONT DE NEMOURS AND COMPANY
1007 MARKET STREET
                                                                                                                                                                                                                                                        UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                  SHARON LPRETTA HAYNIE
VENTION: NOVEL ANTIMICORBIAL COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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83.3%;
                                                                                        08/082,852
                                                                                                                                             US/08/569,188
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Pred. No.
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Best Local :
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Local

10;

Similarity 83., 10; Conservative

76.9%; 83.3%;

Score 40; Pred. No.

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Length 16; Indels

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Gaps

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1 KLLLKLLKILK 12

KKLLKLLKKLLK 15

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; TOPOLOGY: un; MOLECULE TYPE: US-08-569-188-10
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Best Local Similarity 83.38,
Matches 10; Conservative
                                                                                                                  APPLICATION NUMBER: 08/082,85:
FILING DATE: JUNE 22, 1993
ATTORNEY_AGENT INFORMATION:
REGISTRATION NUMBER: 33,692
REFERENCE_POCKET NUMBER: CR-9.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
                                                                                            TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: unknown; MOLECULE TYPE: peptide US-08-569-188-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10, Application Patent No. 5847047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION: APPLICANT: SHARON
                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 525
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD FOR WINDOWS 95 (7.0)
CURRENT APPLICATION DATA:
                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
                                        STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1007 MAR.
CITY: WILMINGTON
STATE: DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: UZIP: 19898
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                                              amino acids
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                          unknown
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            peptide
                                      unknown
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83.3%;
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Pred. No.
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1.7;
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US-08-69-188-12; Sequence 12, Application US/08569188; Patent No. 5847047; PATENT NO. 5847047; GENERAL INFORMATION:
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Best Local S
Matches 10
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                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFÉRENCE/DOCKET NUMBER: CR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
TELEPHONE: 302-773-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: MICROSOFT WO CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: LVU,
CITY: WILMINGTON
STATE: DELAWARE
TMITTED S
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NAME: LINDA AXAMETHY FLOYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/082,852
FILING DATE: JUNE 22, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                              APPLICANT: SHARON LPRETTA HAYNIE
TITLE OF INVENTION: NOVEL ANTIMICORBIAL COMPOSITIONS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD FOR WINDOWS 95 (7.0)
                                                                                                              COUNTRY:
                                                                                                                                                 ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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VENTION: NOVEL ANTIMICORBIAL COMPOSITIONS
                                                                                                              UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Pred. No.
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1.7;
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Best Local Similarity
Matches 10; Conserv
                                                   Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application PC/TUS9407019 GENERAL INFORMATION:
                                                                                                                                                                                                                      APPLICATION NUMBER: 08
FILING DATE: JUNE 22,
INFORMATION FOR SEQ ID NO:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                              COMPUTER: MACINTOSH
OPERATING SYSTEM: MACINTOSH 6.0
SOFTWARE: MICROSOFT WORD, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/070
                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NOVEL /
TITLE OF INVENTION: COMPOS:
NUMBER OF SEQUENCES: 15
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: LINDA AXAMETHY FLOYD REGISTON NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                        TOPOLOGY: ur
MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                  LENGTH: 16 amino acids TYPE: amino acid STRANDEDNESS: unknown
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TOPOLOGY: un
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          1 KLLLKLLKKLLK 12
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KKLLKLLKKLLK 15
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                                                                    76.9%;
83.3%;
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83.3%;
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Pred. No.
                                                                     Pred.
                                                                              Score 40;
                                                     Mismatches
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                                                                     No.
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1.7
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PCT-US94-07019-10
; Sequence 10, Application PC/TUS9407019

RESULT

SENERAL INFORMATION:

FITLE OF INVENTION: NUMBER OF SEQUENCES:

NOVEL ANTIMICROBIAL COMPOSITIONS

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RESULT 10
PCT-US94-07019-12
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PCT-US94-07019-11
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                                                                                                                 Query Match 76.9%;
Best Local Similarity 83.3%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11, Applicat GENERAL INFORMATION:
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Best Local Similarity 83:

Matches 10; Conservative
                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/082
FILING DATE: JUNE 22, 1993
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                           TOPOLOGY: unknown MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US94/07
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/082,852
APPLICATION NUMBER: 08/082,852
FILING DATE: JUNE 22, 1993
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 1
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: MACINTOSH 6.0
OPERATING SYSTEM: MACINTOSH 6.0
SOFTWARE: MICROSOFT WORD, 4.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NOVEL ANTIMICROBIAL TITLE OF INVENTION: COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                   LENGTH:
TYPE: a
                                                        4 KKLLKLLKKLLK 15
                                                                                     1 KLLLKLLKLLK 12
                                                                                                                                                                                                                                             TENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: ur
MOLECULE TYPE:
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SOFTWARE: MICROSOFT WORD, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
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TYPE: amino acid
STRANDEDNESS: unknown
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83.3%;
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                                                                                                                                                                                                                                                                                                                                     08/082,852
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                                                                                                                             Score 40; DB 5;
Pred. No. 1.7;
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Pred. No. 1
                                                                                                                 Mismatches
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RESULT 11
US-08-569-188-3
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APPLICATION NUMBER: PCT/US94/07019
PRIOR APPLICATION NUMBER: PCT/US94/07019
PRIOR APPLICATION NUMBER: 08/082,852
PILING DATE: JUNE 22, 1993
INFORMATION FOR SEO ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
Typp:
                                                            PRIOR APPLICATION NUMBER: 08/082,852
APPLICATION NUMBER: 08/082,852
FILING DATE: JUNE 22, 1993
ATTORNEY/ACENT INFORMATION:
NAME: LINDA AXAMETHY FLOYD
REGISTRATION NUMBER: 3,692
REFERENCE/DOCKET NUMBER: CR-9295-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-8112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CT-US94-07019-12
                                  TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 76.9%;
Best Local Similarity 83.3%;
Matches 10; Conservative
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                            MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IDM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD FOR WINDOWS 95 (7.0)
CURRENT APPLICATION DATA:
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MEDIUM TYPE: DISKETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NO NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 525
                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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MEDIUM TYPE: FLOPPY DISK
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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OPERATING SYSTEM: MACINTOSH
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RY: UNITED STATES OF AMERICA
19898
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1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHARON LPRETTA HAYNIE
ENTION: NOVEL ANTIMICORBIAL COMPOSITIONS
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Pred. No. 1
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1.7;
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RESULT 13
US-08-818-252-39
; Sequence 39, Application US/08818252B
; Patent No. 6197928
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                              US-08-818-253-39
                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 0725
TELECOMMUNICATION INFORMATION:
TELEPAX: 619/678-5070
TELEPAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 39:
                                                                                                                                                                     Query Match
Best Local Similarity
Matches 10; Conserv
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Best Local Similarity 83.3%;
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APPLICANT: Miyawaki, Atsushi
APPLICANT: Miyawaki, Atsushi
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: DETECTION OF ANALYTES
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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FILING DATE: 14-MAR-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                            TOPOLOGY: li
                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
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92037
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SYSTEM: Windows 95
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Pred. No. 1.8;
0; Mismatches
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      CORRESPONDENCE ADDRESS:
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APPLICANT: Tsien, Roger Y.
APPLICANT: Miyawaki, Atsushi
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: DETECTION OF ANALYTES
FILE REFERENCE: 07257/042001
CURRENT APPLICATION UNMBER: US/08/818,252B
CURRENT FILING DATE: 1997-03-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 39
LENGTH: 17
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Best Local Similarity
Watches 10; Conserve
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; FEATURE:
; OTHER INFORMATION: Calmodulin binding peptide-2
US-08-818-252-39
                                                                                                          US-08-569-188-5
                                                                                                                                                                                                                                                                                                                                                  PCT-US94-07019-3
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                                                                    Sequence 5, Application US/08569188 Patent No. 5847047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/082,852
FILING DATE: JUNE 22, 1993
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                    GENERAL INFORMATION: APPLICANT: SHARON
                                                                                                                                                                                                                                                                                                                                                            TENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: MACINTOSH 6.0 SOFTWARE: MICROSOFT WORD, 4.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NOVEL A
TITLE OF INVENTION: COMPOSI
NUMBER OF SEQUENCES: 15
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
TITLE OF INVENTION: NOVEL ANTIMICORBIAL COMPOSITIONS NUMBER OF SEQUENCES: 18
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                                    SHARON LPRETTA HAYNIE
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83.3%;
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83.3%;
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Pred. No. 1.8;
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COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.50 INCH

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: MICROSOFT WINDOWS 95

SOFTWARE: MICROSOFT WORD FOR WINDOWS 95 (7.0)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,188

FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/082,852

PRIOR APPLICATION NUMBER: CR-9295-A

FILING DATE: JUNE 22, 1993

ATTORNEY/AGENT INFORMATION:
NAME: LINDA AXAMETHY FLOYD
REGISTRATION UNUMBER: CR-9295-A

TELEPOMMUNICATION INFORMATION:
TELEPIAN: 302-892-8112

TELEFAX: 302-773-0164

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TTYPE: amino acids
TTYPE: amino acids
TTYPE: amino acids
TTYPE: unknown

MOLECULE TYPE: peptide

US-08-569-188-5
Search completed: June 17, 2002, 12:42:03 Job time: 223 sec
                                                                                                                                                                                                   Query Match 76.9%; Score 40; DB 2; Length 18; Best Local Similarity 83.3%; Pred. No. 1.9; Matches 10; Conservative 0; Mismatches 2; Indels
                                                                                                       1 KILLKILKKIK 12
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6 KKILKILKKILK 17
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STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
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Result
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Maximum DB
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Perfect score:
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2: SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT:*

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Gapop 10.0 ,
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GenCore version 4.5 Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KLLLLK 6
                                                                                                                                                                                                                                                                                                                                                                               /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA199.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA199.DAT:*
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AAB172156
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AAW45766
AAW45166
AAW35166
AAW82813
AAB177381
AAW15767
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             Leu/Lys diastereom
Antipathogenic pep
Antipathogenic pep
Antipathogenis pep
KL-4 pulmonary sur
KL-4 pulmonary sur
Leu/Lys diastereom
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Antipathogenic pep
Antipathogenic pep
KL-4 pulmonary sur
Lytic peptide with
                                                                                                                                                                                                                  Description
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24	24	24	24	24	24	24	24	24	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26
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187	187	187	145	145	80	66	4 3	16	2431	388	311	307	259	258	197	171	136	133	125	121	64	64	39	35	34	21	21	21	21	21	21	21	21
22	22	21	22	22	21	18	22	17	13	21	22	21	21	21	21	20	22	22	22	19	21	19	21	21	21	22	22	21	21	20	19	18	14
AAB85575	AAU29236	AAY66677	AAU21748	AAU23303	AAB24480	AAW28160	AAU17726	AAW07285	AAR25138	AAG46587	AAB80628	AAG06829	AAG55599	AAG55600	AAG55601	AAY37473	AA013335	AAO00228	ABG19410	AAW80409	AAY87304	AAW85466	AAB28015	AAB08290	AAB34780	AAB46100	AAB49683	AAY88039	AAB06344	AAW82278	AAW45763	AAW32109	AAR30661
Human glutathione	Human PRO polypept	Membrane-bound pro	Novel human neopla	Novel human enzyme	Human secreted pro		Novel human respir	Amphiphilic antimi	SFV4 non-structura	Arabidopsis thalia	Environmental stre			Arabidopsis thalia	dopsis	Amino acid sequenc			Novel human diagno	A secreted protein	Human signal pepti	Secreted protein e	secr	H٠	secreted pr	Human surfactant p	Modified surfactan	Respiratory distre	Peptide used in th	Surfactant peptide	KL-4 pulmonary sur	al pulmona	Peptide contg. alt

ALIGNMENTS

AAW35154 RESULT

AAW35154 standard; peptide;

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14-APR-1998 AAW35154;

(first entry)

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Oren Z,
                                                                                                                                                                                              Leu/Lys diastereomer peptide; infection; therapy; excitatory neurotoxin; Honey bee venom; pardaxin; cytolytic activity; cancer; non-haemolytic; preservative; agricultural produce; bacterial cell lysis agricultural pesticide; cell wall lysis.
                 (YEDA ) YEDA RES & DEV CO LTD
                                                                                                                             Misc-difference
                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                               Leu/Lys diastereomer peptide [D]-L1,3-K2L4.
                                      22-FEB-1996;
                                                         20-FEB-1997;
                                                                             28-AUG-1997
                                                                                               WO9731019-A2
                                                                                                                                               Misc-difference
 Shai Y;
                                      96IL-0117223.
                                                         97WO-IL00066.
                                                                                                                                                 Location/Qualifiers
                                                                                                                   /note=
                                                                                                                                      /note= "D-form residue"
                                                                                                                   "D-form residue
                                                                                                                                                                                                          bacterial cell lysis;
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Peptide(s) having selective cytolytic activity - against pathogens and malignant cells, but no haemolytic activity, used for treating

cancer

1997-435088/40

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC This sequence represents a Leu/Lys diastereomer peptide of the CC invention. The peptides of the invention have: (a) cytolytic activity on the peptides of the invention have: (a) cytolytic activity on the cells (pathogenic cells (pathogenic and malignant cells not naturally present in CC concentration significantly higher than that at which they lyse concentration significantly higher than that at which they lyse concentration significantly higher than that at which they lyse concentration significantly higher than that at which they lyse concentrations (caused by bacteria, fungi, protozoa, mycoplasma or viruses) or cancer, in human and veterinary medicine. Also, they can be used as CC cancer, in human deveterinary medicine. Also, they can be used as CC agricultural posticides. The absence of haemolytic activity (associated convented in the control of alpha-helical structures) means that the peptides concreased resistance to proteolytic degradation. Non-haemolytic, cytotoxic random copolymers of pardaxin, each has a specific spectrum of activity, allowing selection of agents for particular applications. Since cresistance to them is unlikely to develop.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
      New non-haemolytic cytolytic agent useful in treating cancer or infections - is a peptide comprising a moiety which disrupts the continuity of an alpha-helical structure
                                                                     WPI; 1998-594464/50
                                                                                                                                (YEDA ) YEDA RES & DEV CO LTD
                                                                                                                                                                                            19-FEB-1998;
                                                                                                                                                                                                                                                                                                       Non-haemolytic; cytolytic; selective cytolytic activity; pathogen; cancer; infection; disinfectant; contact lens wetting solution; preservative; pesticide; fungicide; bactericide.
                                                                                                                                                               20-FEB-1997;
                                                                                                                                                                                                                        27-AUG-1998
                                                                                                                                                                                                                                                     W09837090-A1
                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                        Antipathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW82852 standard; peptide; 6 AA
                                                                                                                                                                                                                                                                                                                                                                                                      19-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW82852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
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                                                                                                                                                            97WO-IL00066.
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Pred. No.
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6.4e+05;
hes 0;
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AAB17418
ID AAB1
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Best Local Similarity
"~+~hes 6; Conserv:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present peptide is used to produce the agents of the invention. The CC specification describes a non-haemolytic, cytolytic agent, which is a peptide, a complex of bundled peptides, a mixture of peptides or a random CC peptide copplymer. The agent has a selective cytolytic activity on CC pathogenic cells. The agent is selected from a cyclic derivative of a CC peptide which has a net positive charge greater than 1, comprises L-amino CC congrises in a peptide (or cyclic derivative of this) which CC (comprises I-amino acid residues and comprises an alpha-helix CC (comprises I-amino acid residues and comprises an alpha-helix CC (comprises I-amino acid residues and Damino acid residues, has a net CC including amino acid sequence comprising only I-amino acid residues is not found in nature. The cytolytic agents may be used for treatment of cancer or for treatment of several diseases caused by pathogens, CC including bacterial, fungal, viral, mycoplasma and protozoan infections. They may be used in both human and veterinary medicine. They may also be cosmetic and food industries, as pesticides (e.g. fungicides or cosmetic and food industries, as pesticides (e.g. fungicides or bactericides) or for preservation of agricultural products.
                                                                              WPI; 2000-350702/30
                                                                                                                                                                               23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                                25-OCT-1999;
                                                                                                                                                                                                                                                               04-MAY-2000
                                                                                                                                                                                                                                                                                                W0200024782-A2
                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                             asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                     Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
                                                                                                                                                (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                           MMP; inhibitor; erythropoietin; cytotoxic T cell lymphocyte ant
                                                                                                                                                                                                                                                                                                                                                                      cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antipathogenic peptide sequence SEQ ID NO:522.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB17418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB17418 standard;
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1 kllllk 6
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                                                                                                             Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 26; Di
ilarity 100.0%; Pred. No. 6.,
Conservative 0; Mismatches
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                                                                                                                                                                               98US-0105371.
99US-0428082.
                                                                                                                                                                                                                              99WO-US25044
                                                                                                               Cheetham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide;
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                                                                                                             Boone
                                                                                                                                                                                                                                                                                                                                                                                         thrombopoietin; interleukin 1; iden 4: tumour necrosis factor;
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hes 0;
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cancer

and

Claim

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Page 379;

608pp; English.

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RESULT
AAW45766
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA694 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes composition of matter (I) comprising FC domain, pharmacologically active peptides, and linkers. Where (I) (X1)a-F1-(X2)b, where: FI = an FC domain; X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of
             Abdel-magid AF,
Villani FJ;
                                                                                                                11-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                      Liquid phase peptide synthesis; KL-4 pulmonary surfactant protein; coupling; respiratory distress syndrome; saponification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently 0 or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
                                                                                    17-JUL-1996;
                                                                                                                                            22-JAN-1998
                                                                                                                                                                        WO9802461-A2
                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                 KL-4 pulmonary surfactant protein precursor peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW45766;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW45766 standard; peptide; 8
                                                        (ORTH ) ORTHO PHARM CORP
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1 kllllk 6
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                                                                                   96US-0021455
                                                                                                              97WO-US12163
                           Eggmann U,
                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                            /note=
                                                                                                                                                                                                                                                                                                                      /note=
                                                                                                                                                                                                                    /note≖
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                                                                                                                                                                                                                                                                                                  "N-terminally modified by t-butyloxycarbonyl
                                                                                                                                                                                                   "Leu-OR, where R is 1-8C alkyl or pheny: 1-8C alkyl"
                                                                                                                                                                                                                                                            "Side chain amino
                                                                                                                                                                                                                                          Side chain amino group of Lys6 protected benzyloxycarboxyl group"
                                                                                                                                                                                                                                                                                     group. Side chain amino
benzyloxycarbonyl group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                         Maryanoff CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA.
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Pred. No.
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hes 0;
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                           Thaler
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CC This peptide is used in a novel process for the synthesis of a KL-4 CC pulmonary surfactant protein. The process comprises: (a) reacting a CC 3-amino acid peptide residue of formula H-Lys(Z)-Leu-Leu-OH with a 5-CC amino acid peptide residue Boc-Leu-Lys(Z)-Leu-Leu-OH (II) to yield CC an 8-amino acid peptide to form an 18-amino acid peptide of formula CC H-Leu-Leu(Lys(Z)-Leu-Leu(Lys(Z)-Leu-Leu)-OH (III) to yield CC peptide with a 3-residue amino acid peptide of formula H-Leu-Leu-CC Lys(Z)-OBzl (X) to form the protected 21-amino acid KL-4 protein; and CC (c) removing the protecting group of the 21-amino acid KL-4 protein by reaction with a suitable acid to form the final KL-4 protein. The CC the synthetic pulmonary surfactant KL-4 which can be used in the CC the synthetic pulmonary surfactant KL-4 which can be used in the CC treatment of respiratory distress syndrome. The saponification process can provide for the deprotection of a peptide ester protected carboxyl CC control of the protect form the final KL-4 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Preparation of KL-4 pulmonary surfactant - using liquid phase peptide synthesis procedures by coupling appropriate peptide fragments
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; Page 27; 30pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-110531/10
                                              provide advantages
  8 AA;
                                              in solubility and control over unwanted by-products
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AAW45768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
17-JUL-1996;
                            11-JUL-1997;
                                                         22-JAN-1998
                                                                                    WO9802461-A2
                                                                                                                                                            Modified-site
                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                   coupling;
                                                                                                                                                                                                                                                                                                                                 Liquid
                                                                                                                                                                                                                                                                                                                                                               KL-4 pulmonary surfactant protein precursor peptide
                                                                                                                                                                                                                                                                                                                                                                                           19-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                        AAW45768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW45768 standard; peptide; 8 AA
                                                                                                                                                                                                                                                 Modified-site
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1 kllllk 6
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nes 6; Conserv
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                                                                                                                                                                                                                                                                                                                    phase peptide synthesis; KL-4 pulmonary surfactant protein;
ng; respiratory distress syndrome; saponification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
 96US-0021455
                              97WO-US12163
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                                                                                                                                             /note=
                                                                                                                                                                                       /note=
                                                                                                                                                                                                                                  /note=
                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                 "N-terminally modified by t-butyloxycarbonyl group"
                                                                                                                                            "Side chain amino group of Lys8 protected
                                                                                                                                                                     "Side chain amino group of Lys3 benzyloxycarboxyl group"
                                                                                                               benzyloxycarboxyl group. C-terminally modifed by OBzl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 26;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 19;
6.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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                                                                                                                                                                                      protected
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(ORTH) ORTHO PHARM CORP

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RESULT
AAW35166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This peptide is used in a novel process for the synthesis of a KL-4 CC 3-amino acid peptide residue of formula H-Lys(Z)-Leu-Leu-OH with a 5-CC amino acid peptide residue Boc-Leu-Lys(Z)-Leu-Leu-OH with a 5-CC an 8-amino acid peptide residue, which is successively reacted with the CC H-Leu-Leu(Lys(Z)-Leu-Lys(Z)-DEDI (III)) to yield CC F-amino acid peptide to form an 18-amino acid peptide of formula CC H-Leu-Leu(Lys(Z)-Leu-Lys(Z)-DEDI (III)) to yield CC H-Leu-Leu(Lys(Z)-Leu-Lys(Z)-DEDI (III)) reacting the 18 amino acid peptide of formula CC peptide with a 3-residue amino acid peptide of formula H-Leu-Leu-CC (c) removing the protecting group of the 21-amino acid KL-4 protein; and CC reaction with a suitable acid to form the final KL-4 protein. The CC methods can be used for the preparation of the polypeptide component of CC treatment of respiratory distress syndrome. The saponification process group with reduced racemisation of a peptide ester protected carboxyl provide advantages in solubility and control over unwanted by-products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
W09731019-A2
                                                           Misc-difference
                                                                                   Misc-difference
                                                                                                             Misc-difference
                                                                                                                                       Misc-difference
                                                                                                                                                                              Synthetic
                                                                                                                                                                                    Leu/Lys diastereomer peptide; infection; therapy; excitatory neurotoxin; Honey bee venom; pardaxin; cytolytic activity; cancer; non-haemolytic; preservative; agricultural produce; bacterial cell lysis agricultural pesticide; cell wall lysis.
                                                                                                                                                                                                                                                           Leu/Lys diastereomer peptide [D]-L3,4,8,10-K3L9.
                                                                                                                                                                                                                                                                                                   14-APR-1998
                                                                                                                                                                                                                                                                                                                                             AAW35166 standard; peptide;
                                                                                                                                                                                                                                                                                                                            AAW35166;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Preparation of KL-4 pulmonary surfactant - using liquid phase peptide synthesis procedures by coupling appropriate peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
les 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-110531/10
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Villani FJ;
                                                                                                                                                                                                                                                                                                                                                                                                                       ω
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KLLLLK 6
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                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                             /note=
10
                                   /note= "D-form residue"
12
                                                                                                                                         Location/Qualifiers
                                                                                                /note=
                                                                                                                          /note≃
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eggmann U,
               "C-terminal amide"
                                                                  "D-form
                                                                                          "D-form residue"
                                                                                                                   "D-form residue"
                                                                                                                                                                                                                                                                                                                                               12
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 26; DB
Pred. No. 6.4
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maryanoff CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 19;
6.4e+05;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thaler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                 bacterial cell lysis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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DT
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XX
XX
XX
XX
XX
PN
PN
PR
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XX
                                                                                                                                                                                                                                                      AAW82883
ID AAW8
                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
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                                                                                                                                                                                                                                                                                                                                      Qy
                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents a Leu/Lys diastereomer peptide of the CC invention. The peptides of the invention have: (a) cytolytic activity on the body; but (b) no haemolytic activity, or such activity only at a concentration significantly higher than that at which they lyse cc pathogens. The peptides, their complexes and mixtures are used to treat cor cancer, in human and veterinary medicine. Also, they can be used as cc preservatives for food, cosmetics and agricultural produce, or as cc with disturbance of alpha-halical structures) means that the peptides cc with disturbance to protecly a structures) means that the peptides cc increased resistance to proteclytic degradation. Non-haemolytic, cor cytotxic random copolymers of pardaxin, each has a specific spectrum of these random copolymers induce total lysis of bacterial cell walls, xx resistance to them is unlikely to develop.
                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local s
Matches 6
       20-FEB-1997;
                               19-FEB-1998;
                                                                            WO9837090-A1
                                                                                                    Synthetic
                                                                                                                      Non-haemolytic; cytolytic; selective cytolytic activity; pathogen; cancer; infection; disinfectant; contact lens wetting solution;
                                                                                                                                                                      Antipathogenic peptide.
                                                                                                                                                                                                   19-MAY-1999
                                                                                                                                                                                                                             AAW82883;
                                                                                                                                                                                                                                           AAW82883 standard; peptide; 12
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide(s) having selective and malignant cells, but no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3;
                                                                                                                                                                                                                                                                                                            7 klillik 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (YEDA ) YEDA RES & DEV CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-FEB-1996;
                                                                                                                                                                                                                                                                                                                                    1 KLLLLK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-AUG-1997
                                                                                                                                                                                                                                                                            7
                                                                                                                                                                                                                                                                                                                                                             Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                        12
                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 39;
  97WO-IL00066
                          .180007I-0M86
                                                                                                                                                                                                                                                                                                                                                                                                                        ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96IL-0117223.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97WO-IL00066.
                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80pp; English.
                                                                                                                     fungicide; bactericide
                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytolytic activity - against pathogens haemolytic activity, used for treating
                                                                                                                                                                                                                                                                                                                                                                  Score 26; DB
Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                           18;
                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                          Length 12;
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RESULT 8
AAB17412
ID AAB174
XX AAB174
AC AAB174
XX 31+OCT
XX ANGIFI
DE ANTIPA
XX MOGIFI
KW autolm
KW immunc
KW MMP; il
KW Cytotc
KW Cytotc
KW Cytotc
KW Vascul
KW asthma
XX WO200(
XX WO200(
XX JAPAN)
PD 04-MAN
XX 23-OCT
PR 22-OCT
XX 23-OCT
PR 22-OCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                  23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                          Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; II-1; TNF; antagonist MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             used as disinfectants for destruction of microorganisms, i.e. solutions for wetting contact lenses, as preservatives, e.g.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (comprises L-amino acid residues and D-amino acid residues, has a net positive charge greater than 1 and has an amino acid sequence such that a corresponding amino acid sequence comprising only L-amino acid residues; is not found in nature. The cytolytic agents may be used for treatment of cancer or for treatment of several diseases caused by pathogens, including bacterial, fungal, viral, mycoplasma and protozoan infections. They may be used in both human and veterinary medicine. They may also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide which has a net positive charge greater than 1, comprises L-amino acid residues and comprises an alpha-helix breaker molety, or a peptide (or cyclic derivative of this) which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          specification describes a non-haemolytic, cytolytic agent, which is peptide, a complex of bundled peptides, a mixture of peptides or a peptide copolymer. The agent has a selective cytolytic activity on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present pe
specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New non-haemolytic cytolytic agent useful in treating cancer infections - is a peptide comprising a moiety which disrupts continuity of an alpha-helical structure
                                                                                                                                  W0200024782-A2
                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                 AAB17412
                                                                                                                                                                                                                                                                                                                                                                                                                               AAB17412 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3;
                                                                 25-OCT-1999;
                                                                                                                                                                                                                                                                                                                              Antipathogenic peptide sequence SEQ ID NO:516.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bactericides) or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cosmetic and food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pathogenic cells. The agent is selected from a cyclic derivative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (YEDA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KLLLLK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 6; Conserv
                                                                                                                                                                                                 thrombosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 38; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide is used to produce the agents of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RES
                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                  98US-0105371
99US-0428082
                                                                 99WO-US25044
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                industries, as pesticides (e.g. for preservation of agricultural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEV
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fungicides or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                antagonist;
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CC (X1)a-F1-(X2)b, where: F1 = an FC domain; X1 and X2 = are each independently selected from -(L1)c-P1-(L2)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P
AAW45767
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                                                                                                                                                                                                                                                                                                                                           coupling;
                                                                                                                                                                                                                                                                                                                                                                                                   KL-4 pulmonary surfactant protein precursor peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                       19-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW45767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW45767 standard; peptide; 13 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes composition of matter (I) comprising FC domain, pharmacologically active peptides, and linkers. Where (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 39; Page 377; 608pp;
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                                                                       Modified-site
                                                                                                                                                                                                                                                                                                     Synthetic
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                                                                                                                                                                                                                                                                                                                                           peptide synthesis; KL-4 pulmonary surfactant protein;
spiratory distress syndrome; saponification.
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             "Side chain amino group of Lys13 protected benzyloxycarboxyl group. C-terminally modifed by OBz1"
                                                                                                                                               "Side chain amino group of
benzyloxycarboxyl group"
                                                                                                                                                                                                                           "N-terminally
                                                                                         Side chain amino benzyloxycarboxyl
                                                                                                                                                                                                         group"
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Pred. No.
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RESULT
AAW7738
ID AA
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                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local s
                                                                                                                                                                                                                                                                                                                                          Matches
WO9841535-A2
                                Modified-site
                                                                                                    Biologically active peptide; hormone; drug; toxin; lipid bilayer membrane; microorganism; parasite; virus
                                                                                              Synthetic.
                                                         Modified-site
                                                                                                                                               Lytic peptide with alterable function
                                                                                                                                                                                14-DEC-1998
                                                                                                                                                                                                         AAW77384;
                                                                                                                                                                                                                      AAW77384 standard; peptide; 15
                                                                                                                                                                                                                                                                                                                               / Match 100.0%; ; Local Similarity 100.0%; ; les 6; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Preparation of KL-4 pulmonary surfactant - using liquid phase peptide synthesis procedures by coupling appropriate peptide
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Villani FJ;
                                                                                                                                                                                                                                                                                                               1 KLLLLK 6
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                                                                                                                                                                         (first entry)
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15
/note=
                                                               Location/Qualifiers
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               "C-terminal
                                   "Optional N-terminal
                                                                                                                                                                                                                                                                                                                                          Score 26; DB
Pred. No. 18;
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                                  myristyl
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RESULT 11
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Best Local Similarity
Matches 6; Conserve
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                                                                       Modified-site
                                                                                                       Modified-site
                                                                                                                                       Modified-site
                                                                                                                                                                               Liquid phase peptide synthesis; KL-4 pulmonary surfactant protein; coupling; respiratory distress syndrome; saponification.
                                                                                                                                                                                                                  KL-4 pulmonary surfactant protein precursor peptide.
                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                   19-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                          The peptides AAW7376-W77390 can be modified by the method of the invention by substituting at least one amino acid of the peptide to a reaction and replacing other amino acid which is modifiable by acids which are not modifiable by the reaction. The methods can be used drugs, toxins and peptides which act on lipid bilayer membranes. The parts in order to affect the structure or integrity or permeability of a body of the animal or plant or within the cells of the body of the animal or plant or within the cells of the body of the animal or plant or within the cells of the body of the animal or plant or within the cells of the body of the animal
                                                                                                                                                                                                                                                                            AAW45765;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                 1 KLLLLK 6
|||||
| kllllk 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New modified peptide(s) - obtained by substitution with an acid which is modifiable by a reaction and replacing other acids which are not to be modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 13; 33pp; English.
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                                                                                                                                         Location/Qualifiers
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                                                            /note=
                                                                                                    /note= "Side chain amino group of Lys protected
    benzyloxycarboxyl group"
                                                                                            /note-
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     "Side chain amino group of Lys protected benzyloxycarboxyl group and C-terminus
                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 26; DB 100.0%; Pred. No. 21; Live 0; Mismatches
                                          "Side chain amino c
benzyloxycarboxyl
                                                                           "Side chain amino c
benzyloxycarboxyl
benzyloxycarboxyl group modifed by OBzl"
                                                                           group of
                                          group of
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                                                   Lys
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lys(Z)-OBzl (X) to form the protected 21-amino acid KL-4 protein; and (c) removing the protecting group of the 21-amino acid KL-4 protein by reaction with a suitable acid to form the final KL-4 protein. The methods can be used for the preparation of the polypeptide component of the synthetic pulmonary surfactant KL-4 which can be used in the treatment of respiratory distress syndrome. The saponification process can provide for the deprotection of a peptide ester protected carboxyl group with reduced racemisation. The liquid phase peptide processes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1a; Page 25; 30pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-JUL-1996;
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          01-JUN-1992;
                                                                                           Synthetic.
                                                                                                                                   Pulmonary
                                                                                                                                                             Peptide
                                                                                                                                                                                          13-MAY-1993
                                                                                                                                                                                                                                                AAR30661 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H-Leu-Leu(Lys(2)-Leu4)3Lys(2)-OBzl (IIIa); (b) reacting the 18 amino acid peptide with a 3-residue amino acid peptide of formula H-Leu-Leu-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Preparation of KL-4 pulmonary surfactant - using liquid phase peptide synthesis procedures by coupling appropriate peptide
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                                     23-DEC-1992
                                                                                                                                                                                                                      AAR30661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       provide advantages in solubility and control over unwanted by-products
                                                                                                                                                                                                                                                                                                                    1 KLLLLK 6
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3 kllllk 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide is used in a novel process for the synthesis of a KL-4
                                                                                                                                                            contg.
                                                                                                                                   surfactant;
                                                                                                                                                                                                                                                                                                                                                                                                                                             18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ΑF,
                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                         (first entry)
                                                                                                                                                             alternating hydrophobic and hydrophilic regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96US-0021455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97WO-US12163
          92WO-US04537
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                                                                                                                                                                                                                                                peptide; 21
                                                                                                                                                                                                                                                                                                                                                                                        100
                                                                                                                                  phospholipid; respiratory distress syndrome;
                                                                                                                                                                                                                                                                                                                                                                                        . 03
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                                                                                                                                                                                                                                                                                                                                                                         0;
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                                                                                                                                                                                                                                                                                                                                                                                      Score 26;
Pred. No.
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The peptide is an example of a highly generic peptide comprising 10 60 amino acid residues, including a sequence having alternating hydrophobic and hydrophilic amino acid residue regions. When the polypeptide is mixed with a phospholipid a synthetic pulmonary surfactant is formed which has greater surfactant activity than the phospholipid alone. The surfactant is used for the treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polypeptide(s) comprising alternating hydrophobic and hydrophilic residue regions - are useful as pulmonary surfactants for treating respiratory distress syndrome
                                                                                                                                                                                                                                                                                                                                                                                                             AAW32109 standard; peptide;
                               Claim 3; Page 16; 31pp; English.
                                                                 Improved preparation of liposomal pulmonary surfactant - for
treatment of respiratory distress syndrome in premature infants
                                                                                                    WPI; 1997-298058/27.
                                                                                                                                                                          20-NOV-1995;
                                                                                                                                                                                              22-OCT-1996;
                                                                                                                                                                                                                       29-MAY-1997
                                                                                                                                                                                                                                              WO9719108-A1
                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                          monolayer formation;
                                                                                                                                                                                                                                                                                                      Liposomal pulmonary surfactant composition; preparation; respiratory distress syndrome; premature infant; prematu
                                                                                                                                                                                                                                                                                                                                        Liposomal pulmonary surfactant composition polypeptide.
                                                                                                                                                                                                                                                                                                                                                               04-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                      AAW32109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            respiratory distress syndrome (RDS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Page 58; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1993-017902/02.
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                                                                                                                                                (ORTH ) ORTHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KLLLLK 6
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6 kllllk 11
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nes 6; Conserv
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                                                                                                                           CF,
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                                                                                                                          Sampino K,
                                                                                                                                                                                              96WO-US16804
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                                                                                                                                                                                                                                                                                           syndrome; premature infant; premature alveolar air-water interface.
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                                                                                                                           Weber JV;
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31;
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The preparation of liposomal pulmonary surfactant composition ethanolic injection has been improved. The liposomal pulmonary

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RESULT 1
AAM45763
ID AAM4
XX AAM4
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AC AAM4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cc surfactant composition comprises a polypeptide and a phospholipid. cC The present sequence represents the polypeptide for use in the CC Ilposomal pulmonary surfactant composition. The preparation comprises CC exhibits enhanced solubility in ethanol, which comprises: (a) preparing a form of the polypeptide (or a salt or ester), which CC a solution of the polypeptide, salt or ester in a fluorinated alcohol CC density at 450 mm of < 0.06; (c) filtering; and (d) removing the CC fluorinated alcohol to recover solid, soluble polypeptide. The CC fluorinated alcohol to recover solid, soluble polypeptide. The CC fluorinated alcohol to recover solid, soluble polypeptide. The CC formation of a monolayer at the alveolar air-water interface, and by during expiration. The liposomal pulmonary surfactant composition can be used to promote the CC during expiration. The liposomal pulmonary surfactant composition can be used in premature infants and occasionally full term meonates who CC sometimes suffer from respiratory distress syndrome due to the lack of xx sufficient endogenous liposomal pulmonary surfactant.
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Best Local
A novel process for its synthesis comprises: (a) reacting a 3-amino acid peptide residue of formula H-Lys(2)-Leu-Leu-OH with a 5-amino acid peptide residue boc-Leu-Leu-Lys(2)-Leu-Leu-OH (II) to yield an 8-amino acid peptide residue, which is successively reacted with the 5-amino acid peptide to form an 18-amino acid peptide of formula 18-amino acid peptide of formula 18-amino acid peptide of formula peptide with a 3-residue amino acid peptide of formula the 18 amino acid peptide with a 3-residue amino acid peptide of formula the 18 amino acid
                                                                                                                                                                                                                                                                      Claim la; page 25;
                                                                                                                                                                                                                                                                                                                                             Preparation of KL-4 pulmonary surfactant peptide synthesis procedures by coupling
                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-110531/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Abdel-magid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ORTH ) ORTHO PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liquid phase peptide synthesis; KL-4 pulmonary surfactant protein; coupling; respiratory distress syndrome; saponification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09802461-A2
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                                                                                                                                             sequence represents a synthetic KL-4 pulmonary surfactant protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF, Eggmann U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               surfactant protein.
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                                                                                                                                                                                                                                                          30pp; English.
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    using liquid phase appropriate peptide

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peptide

formula H-Leu-Leu-

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C KL4 is a synthetic peptide that can be used in a synthetic pulmonary surfactant of the invention. It is a minic of human construction protein Sp-18. Synthetic pulmonary surfactants comprise one or more phospholipids and a peptide having alternating the protein sp-18 controlled the having alternating groups of the synthetic pulmonary surfactant is used in a claimed method for the synthetic pulmonary surfactant is used in a claimed method for pulmonary lavage of a mammal. Lavage is used to treat respiratory contents, pulmonary inflammation or infection, acute hypoxacmia, persistent foetal circulation, congenital diaphramatic hernia, persistent foetal circulation. The lavage solution removes inflammatory mediators and preserves or restores pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DЬ
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Best Local :
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                                                                                                                                                                                                                                       Claim 44; Page 123; 145pp;
                                                                                                                                                                                                                                                           Pulmonary lavage with dilute surfactant solution at positive end-expiratory pressure - with removal of fluid using short periods of suction, used to treat respiratory distress, e.g. in neonates where caused by aspiration of meconium
                                                                                                                                                                                                                                                                                                                                                                                  Cochrane CG,
                                                                                                                                                                                                                                                                                                                                                                                                                                           28-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                         (SCRI ) SCRIPPS RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Surfactant; pulmonary lavage; inflammation; acute hypoaemia; diaphramatic hernia; respiratory distress syndrome; meconium aspiration syndrome; pneumonia; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-NOV-1998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Surfactant peptide KL4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lys(2)-OBzl (X) to form the protected 21-amino acid KL-4 protein; and (C) removing the protecting group of the 21-amino acid KL-4 protein by reaction with a suitable acid to form the final KL-4 protein. The methods can be used for the preparation of the polypeptide component of the synthetic pulmonary surfactant KL-4 which can be used in the treatment of respiratory distress syndrome. The saponification process can provide for the deprotection of a peptide ester protected carboxyl group with reduced racemisation. The liquid phase peptide processes provide advantages in solubility and control over unwanted by-products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW82278;
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CC function.

XX

SQ Sequence 21 AA;

Query Match
Best Local Similarity 100.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLLLK 6
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Db 1 klllk 6

Search completed: June 17, 2002, 12:41:22

Search completed: June 17, 2002, 12:41:22
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GenCore version 4.5
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OM protein - protein search, using sw mode:

Run on: June 17, 2002, 12:42:57; Search time 46.42 Seconds (without alignments) 12.420 Million cell updates/sec

Perfect score: Title: US-09-367-714A-28 26

Scoring table: Sequence: KLLLLK 6

BLOSUM62 Gapop 10.0, Gapext 0.5

Searched:

283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters:

283138

Minimum DB Maximum DB seq length: 0 length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pir2:*
pir3:* pir1:*

Database :

PIR_71:*

* 3 2 1 pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	o	σı	4	ω	2	_	No.	Result	
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92.3	2	2		92.3	Ņ.	•	2	92.3	2.	92.3	N	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	Match	Query	*
239	217	217	215	215	201	165	146	95	93	80	41	2431	1855	748	889	641	809	542	542	403	392	321	. 305	277	205	126	110	110	Length		
N	N	μ	N	N	N	N	N	N	N	N	N	-	N	N	N	N	N	N	N	N	N	N	N	N	N	N	Ν	N	B		
T41951	H71912	B64600	G71537	A81693	AG1668	A64227	C81036	E95270	S15948	H84974	T07329	MNWVSF	S41649	A60202	S32961	A39961	T18437	E81105	B81910	B71482	A81745	S51395	A70212	AB2461	C87309	в72621	F81868	A47154	Ü		
hypothetical prote	probable oxidoredu	NĀD(P)H-flavin oxi	hypothetical prote	~		hypothetical prote	Z				hypothetical prote	nonstructural poly	DNA polymerase - m	choline O-acetyltr	hypothetical prote	choline O-acetyltr	hypothetical prote	ABC transporter, A	٠	hypothetical prote	~	hypothetical prote	◡	hypothetical prote		cal prot	probable proline-r	ב	Description		•

-		-	42 2					37 2							
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389 2	387 2	386 2	356 2	352 1	346 2	337 2	333 2	330 2	328 2	325 2	294 2	262 2	260 2	244 2	239 2
AH3003	T26735	D42528	T06756	E71092	T13837	T18708	AB2130	AD2082	H75073	T31977	T19055	A99155	E90010	T30358	A81301
penicillin-binding	hypothetical prote	B23R protein - vac	hypothetical prote	hypothetical prote	NADH dehydrogenase	hypothetical prote	iron(III) dicitrat	iron(III) dicitrat	hypothetical prote	hypothetical prote	hypothetical prote	conserved hypothet	hypothetical prote	hypothetical prote	probable anion-upt

ALIGNMENTS

conserved hypothetical protein ylxM - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000

C; Accession: A47154; A69882

R;HOnda, K.; Nakamura, K.; Nishiguchi, M.; Yamane, K. J. Bacteriol. 175, 4885-4894, 1993

A;Title: Cloning and characterization of a Bacillus subtilis gene encoding a homolog A;Reference number: A47154; MUID:93328695
A;Accession: A47154

A;Status: preliminary

A; Molecule type: nucleic acid

A; Residues: 1-110 <HON>

A;Cross-references: GB:D14356; NID:g439700; PIDN:BAA22221.1; PID:g2424968
A;Note: sequence extracted from NCBI backbone (NCBIN:135652, NCBIP:135653)
A;Note: sequence extracted from NCBI backbone (NCBIN:135652, NCBIP:135653)
R;Kunst, F; Ogasawara, N: Moszer, I; Albertini, A.M.; Alloni, G; Azevedo, V.; Ber C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; C; Errington, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, National Control of the C C.; Bron, S.; Broullie, A.; Ehrlich, S.D.; Emmerson, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galicch, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino A;Authors: Lauber J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sckowska, A.; Sea akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchlya T.; Winters, P.; Wipat, A.; Yamanoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili A;Reference number: A69580; MUID:98044033

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A; Accession: A69882

A;Molecule type: DNA A;Residues: 1-110 <KUN> A;Cross-references: GB:Z99112; GB:AL009126; NID:g2633902; PIDN:CAB13470.1; PID:g26339 A;Experimental source: strain 168

A;Gene: ylxM C;Superfamily: hypothetical protein A05_orf102 Genetics:

Query Match
Best Local Similarity
Matches 6; Conserv Conservative 100.0%; Score 26; 100.0%; Pred. No. 0; Mismatches DB 2;

0;

0;

Gaps

0

Length 110; Indels

Вþ Ş 1 KLLLLK 6 |||||| 69 KLLLLK 74 74

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peptidy1-tRNA hydrolase [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 14-Sep-2001
C;Accession: C87309
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg,
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kol
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                   RESULT
C87309
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A; Molecule type: DNA
A; Residues: 1-126 <KAW>
A; Cross-references: DDBJ:AP000061; NID:g5104821;
A; Experimental source: Strain K1
C; Genetics:
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C;Superfamily:
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DNA Res.
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C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: B72621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Title: Complete genome sequence of an aerobic A; Reference number: A72450; MUID:99310339
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A; Residues: 1-110 < PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: A81775; A; Accession: F81868
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: Complete DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Holroyd, S.; Jagels, K.
Nature 404, 502-506, 2000
                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local
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6, 83-101, 1999
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Ce: serogroup
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31775; MUID:20222556
                                                                                                                                                                                                                                                                                                                                                                                                                                                               pernix hypothetical protein
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Pred. No. 41;
); Mismatches
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Pred. No. 36;
D; Mismatches
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36;
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Tanaka,
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                                                                                                                                                                                                                                                                                                                                                                                                     Length 126;
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.; Yamazaki,
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                                                                                                                  A; Molecule type: DNA
A; Residues: 1-305 <K
                                                                                                                                                                                    A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic.sequence of a Lyme disease spirochaete,
A;Reference number: A/0100; MUID:98065943
                                                                                A; Experimental source:
                                                                                                  A; Cross-references:
                                                                                                                                           A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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A; Experimental source:
C; Genetics:
                                                                                                                                     Nakazaki, N.; Shimpo, S.;
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-205 <STO>
A;Cross-references: GB:AE005673; NID:g13421661; PIDN:AAK22471.1; GSPDB:GN00148
C;Genetics:
A;Gene: CC0484
C;Superfamily: peptidyl-trNA hydrolase
                                                       A; Molecule type: DNA
A; Residues: 1-277 < KUR>
                                                                                                                                                                                  C;Accession: AB2461
R;Kaneko, T.; Nakamura,
                                                                                                                                                                                                                                                                                                                                                                                                Query Match.
Best Local Similarity
"""" 6; Conserv
                     A;Cross-references: GB:BA000019; PIDN:BAB76941.1; PID:g17134381; GSPDB:GN00179
A;Experimental source: strain PCC 7120
                                                                                       A; Status: preliminary
                                                                                                        A; Reference number: AB1807; A; Accession: AB2461
                                                                                                                                                                                                               A:Note: Anabaena sp. (strain PCC 7120)
C:Date: 14-Dec-2001 #sequence_revision
                                                                                                                                                                                                                                                                  hypothetical protein alr5242 [imported] -
                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                 Species: Anabaena sp.
alr5242
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                                                                                                                                                                                                          (strain PCC 7120) is a synonym of Nostoc sp. strain PCC sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
                                                                                                                                                                  S.; Sugimoto,
                                                                                                                                                                                  Y.; Wolk, C.P.;
                                                                                                             Sequence of the Filamentous Nitrogen-fixing Cyanobacterium 7; MUID:21595285; PMID:11759840
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Pred. No.
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Query Match
Best Local s
Matches 6
66
              1 KLLLLK 6
KLLLLK
                              Similarity 6; Conserv
71
                             100.0%; llarity 100.0%; Conservative 0
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                                   Score 26;
Pred. No.
                           Pred. No. 86;
Mismatches
                                          2;
                            0,
                                          Length 277;
                           Indels
                          0,
                          Gaps
                          0;
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C;Accession: A70212

R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hat Nature 390, 580-586, 1997
                                                                                                                                                                                        conserved hypothetical protein BBA41 - Lyme disease spirochete plasmid A/1p54 C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999 C;Accession: A70212
                                                                     ra, R.;
on, M.;
Hatch,
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A70212

Borrelia burgdorferi

₩ħ B.

VK LEV

GB:AE000790; NID:g2690224; PIDN:AAC66251.1; ce: strain B31

PID:g2690250;

TIGR:BB

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hypothetical protein YLR257w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein L8479.9
C;Species: Saccharomyces cerevisiae
C;Date: 05-May-1995 #sequence_revision 12-May-1995 #text_change 05-Nov-1999
C;Accession: S51395
R;Miller, N.
                         RESULT
B71482
                                                                                                                                                                                                 A; Gene: TC0068
C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                               C:Species: Chlamydia muridarum, Chlamydia tra
C:Date: 31-Mar-2000 #sequence_revision 31-Mar
C:Accession: A81.745
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
A81745
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Best Local Similarity
""" 6; Conserv
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A;Accession: S51395
                                                                                 B
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                                                                                                                                                                                                                                                                                                                             C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Nucleic Acids Res. 28, 1397-1406, 200 A;Title: Genome sequences of Chlamydia trachomatis A;Reference number: A81500; MUID:20150255
                                                                                                                                                                                                                                                                                                                                                                                                           conserved hypothetical protein TC0068 [imported] - Chlamydia muridarum (strain C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 18-Aug-2000
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hypothetical protein C; Species: Chlamydia
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A; Residues: 1-392 <TET>
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A; Status: prelimina
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A; Residues: 1-321 <MIL>
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            strain UW3/Cx)
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R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; ri, H.; Oin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Science 287, 1809-1815, 2000
Science 287, 1809-1815, 2000
A; Authbors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; A; Authbors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.;
A; Reference number: A; Accession: E81105
                                                                                                                                            ABC transporter, ATP-binding protein NMB1240 [imported] - C;Species: Neisseria meningitidis C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_cC;Accession: E81105
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Best Local Similarity
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C;Superfamily: unassigned ATP-binding cassette proteins;
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A; Cross-references: GB:AL162755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491 A;Reference number: A81775; MUID:20222556 A;Accession: B81910
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C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
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"""hes 6; Conserv
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C;Superfamily: conserved hypothetical protein CP0072
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A;Experimental source: serotype I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 18-Aug-2000 C;Accession: B71482 R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, Science 282, 754-759, 1998
                                 A; Title: Complete genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: serogroup
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A; Residues: 1-403 < ARN>
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MUID:20175755
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A, strain Z2491
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S.; Moule,
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                                   serogroup B
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Quail, M.A.;
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                                                                                         K.E.; Eisen,
Dougherty, B.
Pizza, M.
                                     Rappuoli, R.;
strain MC58.
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Rajandre
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A;Status: preliminary A;Molecule type: DNA

C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding

cassette homology

PID: 972264

A;Residues: 1-542 <TET>
A;Cross-references: GB:AE002472; GB:AE002098; NID:g7226475; PIDN:AAF41621.1;
A;Experimental source: serogroup B, strain MC58

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A; Molecule type: DNA
A; Residues: 1-22 <HER>
R; Braun, A.; Barde, Y.A.; Lottspeich, F.; Mewes, W.; Thoenen,
J. Neurochem. 48, 16-21, 1987
A; Title: N-terminal sequence of pig brain choline acetyltransf
A; Reference number: A28047; MUID:87085562
                                                                                                                   A;Cross-references: GB:J03021; NID:g164377; PIDN:AAA31000.1; PID:g164378 R;Hersh, L.B.; Rong, C.F.; Sampson, C.; Mues, G.; Li, Y.P.; Fisher, A.; I. Neurochem. 61, 306-314, 1993 A;Title: Comparison of the promoter region of the human and porcine chol: A;Accession: PH1571; MUID:93294599 A;Status: translation not shown
                                                                                                                                                                                                                                                                                      Choline O-acetyltransferase (EC 2.3.1.6) precursor - pig C; Species: Sus scrofa domestica (domestic pig) C; Date: 08 - Nov-1991 *sequence_revision O8-Nov-1991 *text_change O5-May-2000 C; Accession: A39961; pHI572; A28047; I46574
R; Berrard, S.; Brice, A.; Lottspeich, F; Braun, A.; Barde, Y.A.; Mallet, J. Proc. Natl. Acad. Sci. U.S.A. 84, 9280-9284, 1987
A; Title: cDNA cloning and complete sequence of porcine choline acetyltransferase: A; Accession: A39961; MUID:88097472
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A; Residues: 1-641 <BER>
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Best Local Similarity
"atches 6; Conserve
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A:Accession: T18437
A:Status: preliminary: translated
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R;Lawson, D.; Bowman, S.; Barrell B
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Pred. No. 1.8
0; Mismatches
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Y, August 1997
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Pred. No. 1.6e+02;
Mismatches 0;
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thes 0;
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C;Species: Homo sapiens (man)
C;Date: 10-Nov-1992 #sequence_revision 13-Mar-1997 #text_change 03-Nov-2000
C;Accession: 152631; A60202; S24416; S14483; PH1571; T01786; PC4342; PC4344;
                                                                                                                                         N; Alternate names: choline acetylase
                                                                                                                                                      choline O-acetyltransferase (EC 2.3.1.6) - human
                                                                                                                                                                                          A60202
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C; Superfamily: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                               A/Cross-references: EMBL:Z36128;
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A; Residues: 1-688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: S46140
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A; Residues: 1-688 <DOI>
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A;Title: The complete sequence of a 19,482 bp segment located A;Reference number: $29348; MUID:93220397

A;Accession: $32961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C:Species: Saccharomyces cerevisiae C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 C:Accession: S32961; S46140 R:Doignon, F.; Biteau, N.; Crouzet, M.; Aigle, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: translation not shown
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Best Local Similarity
Matches 6; Conserv
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R;Berrard, S.; Brice, A.E.; Mallet, J.
Brain Res. Bull. 22, 147-153, 1989
A;Title: Molecular genetic approach to the study of mammalian choline acetyltransfera A;Reference number: 146574; MUID:89229974
A;Accession: 146574
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-641 <BE2>
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C;Comment: This enzyme is responsible for the biosynthesis of the neurotransmitter
C:Superfamily: carnitine O-acetyltransferase
C;Keywords: acyltransferase; coenzyme A
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                                             I.; Deguchi, T.
Res. 16, 287-294, 1992
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                      choline acetyltransferase induces two forms
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A; Accession: PC434
A; Molecule type: mRNA
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A;Cross-references: DDBJ:DB2342; NID:g1906789; PIDN:BAA18946.1; PID:d1019687; PID:g19067A;Experimental source: brain
C;Comment: This enzyme is responsible for the biosynthesis of the neurotransmitter acetylcholic;Comment: This enzyme is involved in the synthesis of the neurotransmitter acetylcholic;Comment: This enzyme is involved in the synthesis of the neurotransmitter acetylcholic;Comment: This enzyme is involved in the synthesis of the neurotransmitter acetylcholic;Comment: This enzyme is involved in the synthesis of the neurotransmitter acetylcholic.
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A;Molecule type: mRNA
A;Residues: 111-119,'T',121-260,'GQ',263-391,'A',393-395,'L',397-433,'G',435-528,'S',534
A;Cross references: EMBL:S45018; NID:g257109; PIDN:AAB23557.2; PID:g5705927
R;Misawa, H.; Matsuura, Y.; Oda, Y.; Takahashi, R.; Deguchi, T.
Nol. Brain Res. 44, 323-333, 1997
Nol. Brain Res. 44, 323-333, 1997
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A;Residues: 109-150,'Q',152-232 <TOU>
A;Residues: 109-150,'Q',152-232 <TOU>
A;Residues: 109-150,'Q',152-232 <TOU>
A;Cross references: EMBL:x55685; NID:g29938; PIDN:CAA39923.1; PID:g29939
A;Cervini, R.; Rocchi, M.; DiDonato, S.; Finocchiaro, G.
submitted to the EMBL Data Library, January 1991
A;Description: Isolation and sub-chromosomal localization of a DNA fragmu A;Reference number: S14483
A;Accession: S14483
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A;Note: GenBank sequence 950535 (accession L33837) is
R;Lorenzi, M.V.; Trinidad, A.C.; Zhang, R.; Strauss, W.
DNA Cell Biol. 11, 593-603, 1992
A;Title: Two mRNAs are transcribed from the human gene
A;Reference number: Z14429; MUID:93000480
A;Accession: T01786
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R;Hersh, L.B.; Kong, C.F.; Sampson, C.; Mues, G.; Li, Y.P.; Fisher, A.; Hilt, D.; Baetge J. Neurochem. 61, 306-314, 1993
A;Title: Comparison of the promoter region of the human and porcine choline acetyltrans: A;Reference number: PH1571, MUID:93294599
A;Accession: PH1571
A;Status: translation not shown; translated from GB/EMBL/DDBJ
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A;Title: Human choline acetyltransferase (CHAT): partial gene sequence and potential cora; Reference number: S24416; MUID:92155737
A;Accession: S24416
A;Cross-references: GDB:119775; OMIM:118490
A;Map position: 10q11.2-10q11.2
A;Introns: 129/3; 193/3
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A;Residues: 119 167, 'E',169-256
A;Cross-references: DDBJ:D82340
A;Experimental source: brain
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A; Residues: 119-152 <
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A;Title: Human choline acetyltransferase mRNAs with different 5'-region produce a 69-kD:
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A; Residues: 1-95 <HE2>
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A; Residues: 688-738 <CER>
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C;Superfamily: carnitine O-acetyltransferase
C;Keywords: acyltransferase; coenzyme A
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Query Match 100.0%; Score 26; DB 2; Length 748;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KLLLLK 6
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Db 596 KLLLLK 601
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R;Hersh, L.B.; Takane, K.; Gylys, K.; Moomaw, C.; Slaughter, C.

J. Neurochem. 51, 1843-1845, 1988
A;Title: Conservation of maino acid sequences between human and porcine choline acetyltx
A;Reference number: A60202; MUID:89036242
A;Accession: A60202; MUID:89036242
A;Accession: A60202
A;Molecule type: protein
A;Residues: 'XX',163-182;271-295;340-352;376-382;404-415;550-559;572-583;620-632;644-648
A;Residues: A;Residues

A;Status: translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-748 <RES> A;Cross-references: GB:S56138; NID:g301095; PID:g301096 A;Cross-references: GB:S56138; NID:g301095; PID:g301096 A;Cross-references: GB:S56138; NID:g301095; PID:g301096

Search completed: June 17, 2002, 12:42:59 Job time: 254 sec

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Post-processing: Minimum Maximum
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Y068_CHLMU
Y696_CHLTR
CLAT_PIG
CLAT_YEAST
YFA7_YEAST
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YB8F_YEAST
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ALIGNMENTS

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YLXM_BACSU

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01-OCT-1994 (Rel. 3 01-OCT-1994 (Rel. 3 16-OCT-2001 (Rel. 4 Hypothetical 13.2) P37104; 01-OCT-1994 01-OCT-1994 16-OCT-2001

30, 30, 40, kDa

Created)
Last sequence update)
Last annotation update)
protein in ftsy-ffh intergenic region.

Bacillus subtilis

Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus. NCBI_TaxID=1423;

STRAIN-168; SEQUENCE FROM N.A.

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RESULT 2
YZ10_AQUAE
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MEDLINE-93328695; PubMed-835643;
MEDLINE-93328695; PubMed-83696; 
YZ10_AQUAE
066404;
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EMBL; Z99112; CAB13470.1; -.
PIR; A47154; A47154.
SubtiList; BG10829; ylxM.
Hypothetical protein; Complete proteome.
Hypothetical protein; Complete BDFFEE0A940CD6B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                              Gwinn M., Nelson W., DeBoy R.,
Eisen J., Fraser C.M.;
"Genome sequences of Chlamydia
pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406
                                                                                                                          Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass Linher K., Weldman J., Khouri H., Craven B., Bowman C., Dodson R. Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg
                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=MOPn / Nigg;
MEDLINE=20150255; PubMed=10684935;
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
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NCBI_TaxID=83560;
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P13222;
01-JAN-1990
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Science 282:754-759(1998)
-!- SIMILARITY: BELONGS T
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STRAIN-D/UW-3/CX;
MEDLINE-99000809; PubMed-9784136;
Stephens R.S., Kalman S., Lammel C.J., Fa
Mitchell W.P., Olinger L., Tatusov R.L.,
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16-OCT-2001
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=813;
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SEQUENCE 392 AA; 45694
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L protein CT696.
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Q., Koonin E.
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RESULT 6
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A Berrard S., Brice A., Lottspeich F., Braun A., Ba "cDNA cloning and complete sequence of porcine che acetyltransferase: in vitro translation of the coryline an active protein.";

Proc. Natl. Acad. Sci. U.S.A. 84.0000
                                                                                                                  Query
Best I
                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                            J. Néurochem. 48:16-21(1987).

-I. FUNCTION: Catalyzes the reversible synthesis of acetylcholine
-(ACh) from acetyl CoA and choline at cholinergic synapses.
-I. CATALYTIC ACTIVITY: Acetyl-CoA + Choline = CoA + O-acetylcholine.
-I. SIMILARITY: BELONGS TO THE CARNITINE/CHOLINE ACETYLTRANSFERASE
                                                                                                                                                                           INIT_MET
                                                                                                                                                                                                           Pfam; PF00755; Carn_acyltransf; 1.
PROSITE; PS00439; ACYLTRANSF_C_1; 1.
PROSITE; PS00440; ACYLTRANSF_C_2; 1.
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EMBL; M27736; AAA31015.1;
PIR; A28047; A28047.
PIR; A39961; A39961.
                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed.
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Choline O-acetyltransferase
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                                                                     1 KLLLLK
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                                                           KLLLLK
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Eutheria;
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5ECC27BE8B7CC317
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Best Local S
Matches 6
                                                                                                                SEQUENCE FROM N.A.
TISSUE-Spinal cord;
MEDLINE-93180642; PubMe
Oda Y., Nakanishi I., D
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01-OCT-1994 (Rel. 30
15-JUL-1998 (Rel. 36
Hypothetical 80.4 kD
YBR259W OR YBR1727.
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                                                                     Brain Res. [2]
                                               SEQUENCE
T-305; C-
                                                                                                                                                                                                                                              CLAT_HUMAN STANDARD: PRT; 748 AA. P28329; Q16488; Q9BQE1; Q9BQ35; Q9BQ23; Q1DEC-1992 (Rel. 24, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) Choline O-acetyltransferase (EC 2.3.1.6) (CHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93220397; PubMed=8465606;
Doignon F., Biteau N., Crouzet M., Aigle M.;
"The complete sequence of a 19,482 bp segment located arm of chromosome II from Saccharomyces cerevisiae.";
                                                                                "A complementary DNA for human choline acetyltransferase induces two forms of enzyme with different molecular weights in cultured cells."; Brain Res. Mol. Brain Res. 16:287-294(1992).
                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
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EMBL; Z36128; CAA85222.1;
PIR; S32961; S32961.
SGD; S0000463; YBR259W.
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NCBI_TaxID=4932;
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             Ohno K.,
                        MEDLINE=21117155;
                                     AND G-392
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R., Robb
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K-441;
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A., Brengman J.M.,
S., Kirkham F.J.,
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I., Deguchi T.;
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Mismatches
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  Engel
  Harper C.M.,
Engel A.G.;
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                                               AND H-560,
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                                               FIMG2
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                                                VARIANTS
                                               P-210; A-211;
VARIANTS T-120
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acetyltransferase.

Cell Biol.

11:593-603(1992).

the

SEQUENCE OF 111-669 FROM MEDLINE=93000480; PubMeda-Lorenzi M.V., Trinidad A. Lorenzi M.V., Trinidad A.C., Zha

PubMed=1388731;

N.A

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Cervini R., Rocchi M., DiDonato S., Finocchiaro G., "Isolation and sub-chromosomal localization of a DNA human choline acetyltransferase gene.";
Neurosci. Lett. 132:191-194(1991).

-!- FUNCTION: Catalyces the reversible synthesis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Simoni P., Kempf J.;
"Human choline acetyltransferase (CHAT): partial gene sequence and potential control regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 109-232 FROM N.A.
MEDLINE=92155737; PubMed=1339386;
Toussaint J.L., Geoffroy V., Schmitt M., Werner A., Garnier J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Choline acetyltransferase mutations cause myasthenic syndrome associated with episodic apnea in humans."; Proc. Natl. Acad. Sci. U.S.A. 98:2017-2022(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ACh) from acetyl CoA and choline at choline gic synapses.

- CATALYTIC ACTIVITY: Acetyl-CoA+ choline = CoA+ O-acetylcholine.

- ALTERNATIVE PRODUCTS: 3 isoforms; M/83 kDa (shown here), S/74 kDa and R/70 kDa; are produced by alternative splicing.

- DISEASE: Defects in CHAT are a cause of familial infantile myasthenic gravis type 2 (FIMG2) (also known as CMS-BA). FIMG2 negative tests for anti-AchR antibodies, and abrupt episodic crises with increased weakness, bulbar paralysis, and apnea similarity: BeLONGS TO THE CARNITINE/CHOLINE ACETYLTRANSPERASE TANATTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ween the Swiss Institute of Bloinforma
European Bioinformatics Institute. The
by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the Ew European Bioinformatics Institute. There are no restr by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                      d and this statement is not removed. s requires a license agreement (See an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R., Strauss W.L.;
human gene for choline
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EMBL; AF305905; CAAA39023.1; -
EMBL; X56585; CAAA39023.1; -
EMBL; X56679; CAAA4201.1; -
EMBL; X56679; CAAA4201.1; -
EMBL; S24416; S24416.

R MIM; 114490; -
Th4FFFC: IPR000542; Carn_acyltransf
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CONFLICT
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Pfam; PF00755; Carn_acyltransf; 1.
PROSITE; PS00439; ACYLTRANSF_C_1; 1.
PROSITE; PS00440; ACYLTRANSF_C_2; 1.
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VARIANT 120 120 A -> T.
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/FTIG+VAR_011674.
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RGDPGDVGGPAGNPGCSPHPRAATRPPPLCAHTPAHTPEWC
GAASAEBAEPRA -> MWPECRDEALSTV (IN
SOFORM S).
MISSING (IN ISOFORM R).
R -> Q (IN REF. 1).
GQ -> PE (IN REF. 1).
G -> A (IN REF. 1).
G -> S (IN REF. 3).
G -> S (IN REF. 3).
G -> S (IN REF. 3).
C -> S (IN REF. 3).
EL -> DV (IN REF. 3).
EL -> DV (IN REF. 3).
EL -> DV (IN REF. 3).
T -> M (IN REF. 3).
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V -> L (IN FIMG2; J
/FTId-VAR_011673;
R -> H (IN FIMG2; J
/FTId-VAR_011674.
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R -> G (IN FIMG2;
/FTId=VAR_011671.
S -> L (IN FIMG2;
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Pred.
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/FTId=VAR_011666.
P -> A (IN FIMG2;
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-> M (IN REF. 3)
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TISSUE=Lymphocytes;
MEDLINE=92149876; PubMed=1784419; SEQUENCE OF 688-738 FROM N.A.

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InterPro; IPR002620; Peptidase_C9.
InterPro; IPR001788; RNA_dep_RNApol2.
InterPro; IPR000606; Viral_helicase1.
Pfam; PF01661; Alpp; 1.
Pfam; PF01777; Peptidase_C9; 1.
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PIR; A23592; MNWVSF.
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CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids Res. 14:5667-5682(1986).
-I- FUNCTION: NSP2 MAY BE INVOLVED IN RNA BINDING DURING REPLICATION-II- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE-86286581;
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                                                                                                                                                                                                                                                                                                                                                                                   Ctural protein; RNA-binding; Helicase.
37 NONSTRUCTURAL PROTEIN NSP1.
35 NONSTRUCTURAL PROTEIN NSP2.
17 NONSTRUCTURAL PROTEIN NSP3.
31 NONSTRUCTURAL PROTEIN NSP4.
269286 MW; 1F9EBA1022E3EC5F CRC64;
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Pred. No. 2.7e+02;
Mismatches 0;
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                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-ATCC 33923 / AT-62;
MEDLINE-91238680; PubMed=2034208;
Nishiyama M., Horihouchi S., Beppu T.;
Characterization of an operon encoding succinyl-CoA synthetase and "Characterization of from Thermus flavus AT-62 and its expression in Escherichia coli.";
Mol. Gen. Genet. 226:1-9(1991).
                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=20445173; PubMed=10993077;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa "Genome sequence of the endocellular bacterial symbiont of Buchnera sp. APS.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              symbiotic bacterium).
Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermus aquaticus (subsp. flav
Bacteria; Thermus/Deinococcus
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Pfam; PF01722; BolA; I.
Hypothetical protein; Complete proteome.
SEQUENCE 80 AA; 9299 MW; 4AFACA590A038131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=274;
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    -!- SIMILARITY: BELONGS TO THE YCF81 FAMILY.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
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(Rel. 40, Last annotation update)
protein in SCSB 5'region (ORFA) (Fragment).
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Pred. No. 29;
1; Mismatches
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EMBL; X54073; CAA38004.1;

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AC P52386
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P47487; O1-OCT-1996 (Rel. 34, Created)
O1-OCT-1996 (Rel. 34, Last seque
16-OCT-2001 (Rel. 34, Last seque
                                                                                                                                                                 InterPro; ipR002698; 5-FTHF_cyc-lig.
Pfam; PF01812; 5-FTHF_cyc-lig; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 165 AA; 19355 MW; AEC4ADEEE55A7020 CRC64;
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

STRAIN-ATCC 33530 / G-37;

MEDLINE-96026346; PubMed-569993;

Fraser C.M. Gocayne J.D. White O., Adams M.D., Clayton R.A.,

Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,

Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,

Myuyen D.T., Otterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,

Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucler T.S.,

Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.,

"The minimal gene complement of Mycoplasma genitalium.";

Science 270:397-403(1995).
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                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a chetween the Swiss Institute of Bioinformatics and the EMBL. the European Bioinformatics Institute. There are no restrict use by non-profit institutions at long as its content is entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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Bacteria; Firmicutes;
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InterPro; IPR002792;
Pfam; PF01938; TRAM;
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                                    STANDARD;
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(Rel. 40, Last annotation updat
protein MG245
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83
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83.3%;
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Pred. No.
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                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                     MEDLINE-93139035; PubMed=7678592; Evans D.J., Graham (Evans D.G., Karjalainen T.K., Evans D.J., Graham (Cloning, nucleotide sequence, and expression of adhesin subunit protein of Helicobacter pylori.", J. Bacteriol. 175:674-683(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                        HPA1_HELPY STANDARD; PRT; 260 AA. Q48264; Q48264; Q1-NOY-1997 (Rel. 35, Created) Q1-NOY-1997 (Rel. 35, Last sequence update) Q1-NOY-1997 (Rel. 35, Last sequence update) Q1-NOY-1997 (Rel. 35, Last annotation update) Neuraminyllactose-binding hemagglutinin precursor (N-acetylneuraminyllactose-binding fibrillar hemagglutinin receptor-acetylneuraminyllactose-binding fibrillar hemagglutinin receptor-
                                                                                                                                             -!- PTM: THE N-TERMINUS IS
                                                                                                                                                                                                                                                                                             STRAIN=8826;
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                           Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=210;
                                                                                                                                                                                                                                                                                                                                                                                                                      binding subunit) (NLBH) (Flagellar sheath adhesin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996 (
16-OCT-2001 (
Protein U49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
-- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV
-- EHV-1 37, EBV BXRF1, HCMV UL76, ILTV ORF3, AND VZV 35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human herpesvirus (type 7 / strain JI) (HHV7).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
NCBL_TaxID=57278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. Nicholas J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 KILLLK 29
                                                                                                                                                                   anchor (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KLLLLK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity es 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pro; IPR002580; Herpes_UL24.
PF01646; Herpes_UL24; 1
NCE 239 AA; 28568 MW; F4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U43400; AAC54711.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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40, Last annotation updat
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                                                                                                                                             BLOCKED.
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                                                                                                                                                                     to the outer membrane
         (See http://www.isb-sib.
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DB 1;

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Best Local
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01-FEB-1991 (Rel.
16-OCT-2001 (Rel.
Protein C17/B23.
                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the property of the p
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                                                               REPEAT
REPEAT
                                                                                                                                                                                    InterPro; IPR002110; ANK. Pfam; PF00023; ank; 3. SMART; SM00248; ANK; 1.
                                                                                                                                                                                                                                                                       EMBL; M35027; AAA48222.1; EMBL; M35027; AAA47979.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vaccinia virus (strain viruses, dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
            SEQUENCE
                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                             modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Appendix to 'The complete DNA Virology 179:517-563(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goebel S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPLETE GENOME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Virology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goebel S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-91021027; PubMed-2219722;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Orthopoxvirus
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                             REPEAT
                                           REPEAT
                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Paoletti E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The complete DNA sequence Virology 179:247-266(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Paoletti E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
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                                                                                                                  REPEAT
                                                                                                                                                   PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: CONTAINS 6 ANK REPEATS.
                                                                                                                                                                                                                                      D42528;
F42502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X61574; CAA43773.1;
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5; Conser
                                                                                                                                                 PS50088; ANK_REPEAT; FAL
PS50297; ANK_REP_REGION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PS00013; PROKAR_LIPOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J., Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Outer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          260
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; F42502.
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28
134
                                                                                                                                  Repeat.
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91
126
245
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381
44941
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17,
40,
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83.3%;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Copenhagen).
, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                       .: .:
          MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of vaccinia virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Perkus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1:
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N-ACYL DIGLYCERIDE (PROBABLE).
N-ACETYL-NEURAMINYL-ALPHA(2,3)-LACTOSE
BINDING MOTIF (POTENTIAL).
; 22489598065E7B14 CRC64;
                                         ANK
ANK
ANK
ANK
         ANK 6.
D553A134C9317A42 CRC64;
                                                                                                                                                                 FALSE_NEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              386
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1; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vaccinia virus'.";
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                                                                                                                                                                                                                                                                                                                                                           Usage
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
DNA (cytosine-5)-methyltransferase-like protein 2 (DNA
methyltransferase homolog HsaIIP) (DNA MTase homolog HsaIIP)
                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    014717;
EMBL; AF012128; AAC51939 1; -.
EMBL; AJ223333; CAA11272.1; -.
EMBL; AL133415; CAB87964.1; -.
PDB; 1G55; 17-JAN-01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dong A., Yoder J.A., Zhang X., Zhou L., Bestor T.H., Cheng X.; "Structure of human DNMT2, an enigmatic DNA methyltransferase that displays denaturant-resistant binding to DNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-98258972; PubMed-9599025;
Van den Wyngaert I., Sprengel J., Kass
"Cloning and analysis of a novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  methyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98087580; PubMed=9425235; Yoder J.A., Bestor T.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNM2_HUMAN
                                                                                                                                    entities requires a license agreement (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic Acids Res. 29:439-448(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20580737; PubMed=11139614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEBS Lett. 426:283-289(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fission yeast.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "A candidate mammalian DNA methyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (M.HSaIIP)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KLLLLK 6
                                                                                                                                                                                                                                                                                              TISSUE SPECIFICITY: Ubiquitous.
SIMILARITY: BELONGS TO THE C5-METHYLTRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                              FUNCTION: Seems not be active as a DNA methyltransferase. strong binding to DNA suggests that it may mark specific in the genome by binding to DNA through the specific target
                                                                                                                                                                                                                                                                                                                     recognizing motif.
TISSUE SPECIFICITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (APR-2000) to the EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7:279-284(1998).
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REBASE; MIM; 60:

602478;

IPR001525; C5_DNA_meth

3241; M.HsaIIP.

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DR Pfam; pF00145; DNA_methylase; 2.
DR PRINTS; PR00105; C5METTRERASE_1; FALSE_NEG.
DR PROSITE; PS000094; C5_MTASE_1; FALSE_NEG.
DR PROSITE; PS000095; C5_MTASE_2; 1.

KW DNA-binding; 3D-structure.
FT ACT_SITE 79 79
SQ SEQUENCE 391 AA; 44596 MW; BCA549E4EB2E6950 CRC64;

Query Match
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLLLLK 6
Db 334 KLLILK 339

Search completed: June 17, 2002, 12:44:46

Search completed: June 17, 2002, 12:44:46
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Result
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Q9JUB3
Q9HGZ7
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STRAIN=Y, CN BW SP;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mugall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Yu C., Lewis S.E., Rubin G.M., Celniker S.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AY060401; AAL25440.1; -...
                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

MCBI_TaxID=7227;
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   PRELIMINARY;
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01-NOV-1999
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C., Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T., Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd Jagels K., Leather S., Moule S., Mungall K., Quail M.A., Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrell B.G.; "Complete DNA sequence of a serogroup A strain of Neisseria Nature 404:502-506(2000).

EMBL; AL162756; CAB84951.1; -.
                                                                                                                   crenarchaeon, Aeropyrum pernix K1.";
DNA Res. 6:83-101(1999).
                                                                                Hypothetical SEQUENCE 12
                                                                                                                                                                                                                         MEDLINE=99310339;
                                                                                                                                                                                                                                        STRAIN=K1;
                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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SEQUENCE
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                                                                                                                                                                                                                                                                                            Archaea; Crenarchaeota;
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01-OCT-2000
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MEDLINE=20222556; PubMed=10761919;
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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C STRAIN-ATCC 19089 / CB15;

X MEDILINE-21173698; PubMed-11259647;

X MIERTAIN W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.A.

A Nierman W.C., Feldblyum T.V., Laub M.T., Dulsen I.T., Nelson K.A.

Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Elland R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

A DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry

A Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., Whi

(A Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

Complete genome sequence of Caulobacter crescentus.";

Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
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MCCOmbie W.R.;
MCCOmbie (APR-1999) to the END END ALI63702; CAB87363.1; -
EMBL; ALI63702; CAB87363.1; -
146 146 146 146 16333 MW
InterPro; IPR001328; Pept_trNA_hydro.
Pfam; PF01195; Pept_trNA_hydro; 1.
ProDom; PD005324; Pept_trNA_hydro; 1.
                                         EMBL; AE005721; AAK22471.1; HSSP; P23932; 2PTH. TIGR; CC0484; -.
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01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
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Seeger K., Ha
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Schizosaccharomycetales; Schizosaccharomycetaceae;
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Eukaryota; Fungi; Ascomycota; Schizosacch
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CYTOPLASMIC
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01-OCT-2000 (TrEMBLrel. 1:
01-OCT-2000 (TrEMBLrel. 1:
01-DEC-2001 (TrEMBLrel. 1:
 SEQUENCE FROM N.A. STRAIN=ATCC 35210 / MEDLINE=98065943; p Fraser C.M., Casjen
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MEDLING-20330374; PubMed-10871400;
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01-JUN-1998 (TrEMBLrel. 06, Last
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Bacteria; Spi
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SEQUENCE 265
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SEQUENCE
                                                                                                                                   Borrelia burgdorferi
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Pro; IPR001351; Ribosomal_S3.
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                                                                      STRAIN-S288C (AB972);
Cherry J.M.;
Submitter
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STRAIN-S288C (AB972);
MEDLINE-97313267; PubMed-9169871;
Johnston M., Hillier L., Riles L.
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Submitted (AUG-1997) to tl
EMBL; U17244; AAB67379.1;
SGD; S0004247; YLR257W.
SEQUENCE 321 AA; 35998
                                                                                                                                                                                                               STRAIN=S288C (AB972);
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STRAIN=S288C (AB972);
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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Nature 390:580-586(1997)
                                                                                                                                                                             Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         257
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6; Conservative
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AA; 35998
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  E8E1FC17FFB27418 CRC64;
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Dubois E., Dusterhoft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Hoheisel J.D.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pohl T.M.,
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RESULT
Q9JZ89
ID Q9
AC Q9
DT Q1
RN QN NI
COC N N
RY SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

RC STRAIN-MC58 / SEROGROUP B;

RX MEDLINE-20175755; PubMed-10710307;

RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,

RA Lisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,

RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,

RA Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B.,

RA Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamatheyan J.,

RA Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,

RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;

"Complete genome sequence of Neisscria meningitidis serogroup B Strain
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Best Local S
Matches 6
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Q9JZ89;
01-OCT-2000
01-OCT-2000
01-DEC-2001
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Q9G8N5,
Q9G8N5,
01-MAR-2001 (TrEMBLrel. 16,
01-JUN-2001 (TrEMBLrel. 11,
RIBOSOMAL PROTEIN S4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neisseria meningitidis (serogroup B).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABC TRANSPORTER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The mitochondrial genome of the supposedly primitive protist, Naegleria gruberi.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF288092; AAG17819.1;
InterPro; IPR002942; S4.
Fiam; PF01479; S4; 1.
SMART; SM00363; S4; 1.
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Mitochondrion.
Eukaryota; Heterolobosea;
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) (Tremblrel. 15, L;
l (Tremblrel. 19, L;
l Tremblrel. 19, L;
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16,
17,
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Last sequence update)
Last annotation update)
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Pred. No.
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Pred. No. 1.6
0; Mismatches
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R Pfam; PPO0005; ABC_tran; 2.

SMART; SM00382; AAA; 1.

""D-binding; Complete proteome.

""D-binding; Complete proteome.
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CYTOPLASMIC I
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Best Local S
Matches 6
                                                                                                             Q9HGZ7
Q9HGZ7;
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RMBL; AL162755; CAB84649.1; -.
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InterPro; IPRO03439; ABC_transportr.
InterPro; IPRO01687; ATP_GTP_A.
InterPro; IPR001687; AC_tran; 2.
SMART; SM00382; ABC_tran; 2.
SMART; SM00382; AAA; 1.
STP-binding; Complete proteome.
SEQUENCE 542 AA; 60778 MW; 1EACB1[
                                                                                                                                                                                                                                                     462 KLLLLK
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01-OCT-2000
01-OCT-2000
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Parkhill 1 2054-
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STRAIN=Z2491 / SEF
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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01-OCT-2000 (TrEMBLrel. 15, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
PUTATIVE ABC-TRANSPORTER ATP-BINDING
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EMBL; AE002472; AAF41621.1;
TIGR; NMB1240;
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IPR003439; ABC_transportr.
IPR001687; ATP_GTP_A.
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(TremBLrel. 16, Created)
(TremBLrel. 16, Last sequence update)
(TremBLrel. 19, Last annotation update)
DYNEIN INTERMEDIATE CHAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_1.
PROSITE: PS50082; WD_REPEATS_2; 1.
PROSITE: PS50294; WD_REPEATS_REGION; 1.
Repeat; WD_repeat.
Repeat; WD_repeat.
SEQUENCE 544 AA; 60960 MW; 1057A3C5435
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
HYPOTHETICAL 62.8 KDA PROTEIN.
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                                                                                                                                       Hypothetical SEQUENCE 5
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Pfam; PF00400; WD40; 5. 
SMART; SM00320; WD40; 5.
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NCBI_TaxID=777;
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Coxiella group; Coxiella.
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Pred. No. 2.6
D; Mismatches
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C -!- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY.

R InterPro; IPRO02094; DNA_POL_B.

R Pfam; PF00136; DNA_POL_B; 1.

R Pfam; PF00136; DNA_POL_B = 1.

R Pfam; PF00136; DNA_POL_B = 2.

R PFAMT; SM00486; POLDE; 1.

R PRINTS; PR00106; DNAPOLB.

R PROSITE; PS00116; DNA_POLB-B; 1.

R PS00116; DNA_POLB-B; 1.
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Best Local Similarity
Matches 6; Conserv
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01-DEC-2001
01-DEC-2001
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01-MAY-2000
01-MAY-2000
01-DEC-2001
SEQUENCE FROM N.A.

STRAIN-Y, CN BW SP;

Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.

Champe M., Chavez C., Dorsett V., Farfan D., Frise E., Georg

Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall

Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong S.,

Yu C., Lewis S.E., Rubin G.M., Celniker S.;

Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AY058628; AAL13857.1;

EMBL; AY058628; AAL13857.1;

SEQUENCE 576 AA; 63439 MW; 0588C7F8E07E1249 CRC64;
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MEDLINB=92107655; PubMed=1762904;

Ridley R.G., White J.H., McAleese S.M., Goman M., Alano P.,

de Vries E., Kilbey B.J.;

"DNA polymerase delta: gene sequences from Plasmodium falciparum
indicate that this enzyme is more highly conserved than DNA polym
                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; MuscEphydroidea; Drosophilidae; Drosophila
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Search completed: June 17, 2002, 12:44:20 Job time: 295 sec Matches 6; Conservative 0; Mismatches 1 KLLLLK 6 |||||| 347 KLLLLK 352 0; Indels 0; Gaps 0;

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1: /cgn2_6/ptodata/2,

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Copyright (c) 1993 - 2000 Compugen Ltd.
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Sequence 2, Appli	Sequence 6, Appli	Sequence 12, Appl	Sequence 246, App	Sequence 2, Appli	Sequence 223, App	Sequence 219, App	Sequence 215, App	•	Sequence 223, App								

ALIGNMENTS

PATENT NO. 5613764 GENERAL INFORMATION: APPLICANT: Abdel-Magid, Ahmed F. APPLICANT: Eggmann, Urs APPLICANT: Eggmann, Urs APPLICANT: Maryanoff, Cynthia A. APPLICANT: Thaler, Adrian APPLICANT: Maryanoff, Cynthia A. APPLICANT: Thaler, Adrian APPLICANT: Willani, Frank J. TITLE OF INVENTION: LIQUID PHASE PEPTIDE SYNTHESIS OF KL-4 TITLE OF INVENTION: LIQUID PHASE PEPTIDE SYNTHESIS OF KL-4 TITLE OF INVENTION: DIGNORY SURFACTANT PROTEIN NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS: ADDRESSEE: Johnson & Johnson STREET: One Johnson & Johnson Plaza CITY: New Brunswick STATE: New Jersey COUNTRY: USA ZIP: 08933-003 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/881,971 FILING DATE: CLASSIFICATION DATA: APPLICATION NUMBER: US 60/021,455 FILING DATE: TAULT-1996

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                                      Sequence 5, Application US/08881971 Patent No. 6013764 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION

APPLICATION NUMBER: US/08/881, y/1

FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/021,455

FILING DATE: 17-JUL-1996

ATTORNEY/AGENT INFORMATION:

NAME: DOW, Kenneth J.

NAME: DOW, Kenneth J.
                                                                                                                                                                                                                                                          Matches
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Best Local :
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INFORMATION FOR SEQ ID NO:
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      APPLICANT:
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APPLICANT: Eggmann, Urs
APPLICANT: Maryanoff, Cynthia A.
APPLICANT: Thaler, Adrian
APPLICANT: Villani, Frank J.
TITLE OF INVENTION: FIQUID PHASE PEPTIDE SYNTHESIS OF KL-4
NUMBER OF SEQUENCES: 7
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
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TELEPHONE: 908-524-2641
TELEFAX: 908-524-2808
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Johnson & Johnson
                                                                                                                                                                                                                                              / Match 100.0%; Score 26; DB 3; Local Similarity 100.0%; Pred. No. 1.7e+05; DS 6; Conservative 0; Mismatches 0;
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Abdel-Magid, Ahmed F. Eggmann, Urs
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                                                                                                                                                                                                                                                                                                                                                                   peptide
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                                                                                                                                                                                                                                                                              DB 3; Length 8,
                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                            0;
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US-08-881-971-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08881971 Patent No. 6013764
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Best Local Similarity
Matches 6; Conserv
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INFORMATION FOR SEQ ID NO:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                               APPLICANT: Abdel-Magid, Ahmed F.
APPLICANT: Eggmann, Urs
APPLICANT: Eggmann, Urs
APPLICANT: Maryanoff, Cynthia A.
APPLICANT: Thaler, Adrian
APPLICANT: Villani, Frank J.
TITLE OF INVENTION: LIQUID PHASE PEPTIDE SYNTHESIS OF
TITLE OF INVENTION: PULMONARY SURFACTANT PROTEIN
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Johnson & Johnson
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LENGTH: 13 amino acids
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 6
FILING DATE: 17-JUL-1996
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Johnson & Johnson STREET: One Johnson & Johnson Plaza CITY: New Brunswick
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APPLICANT: Thaler, Adrian
APPLICANT: Villani, Frank J.
TITLE OF INVENTION: LIQUID PHASE PEPTIDE SYNTHESIS OF KL-4
TITLE OF INVENTION: PULMONARY SURFACTANT PROTEIN
                                                                                                                                                                         ADDRESSEE: Johnson & Johnson Plaza CITY: New Brunswick
                                                                                    COUNTRY: USA
ZIP: 08933-003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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                                                                                                                                                             New Jersey
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: FILING DATE:

SOFTWARE:

PatentIn Release #1.0, Version #1.30

US/08/881,971

COMPUTER: IBM PC OPERATING SYSTEM:

IBM PC compatible YSTEM: PC-DOS/MS-DOS

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US-07-715-397A-1
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Best Local Similarity 100.0%;
Matches 6; Conservative (
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INFORMATION FOR SEQ ID NO: 1:
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                             NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                    CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                           COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-BCASE #1.0,
CURRENT APPLICATION DATA:
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LENGTH: 18 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cochran, Charles G
APPLICANT: Revak, Susan D
TITLE OF INVENTION: PULMONARY SURFACTANT PROTEIN AND RELATED
TITLE OF INVENTION: POLYPEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Dow, Kenneth J.
REGISTRATION NUMBER: 32,890
REFERENCE/DOCKET NUMBER: MC
                                                                                                                                                          APPLICATION NUMBER: US
FILING DATE: 19910614
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                                                                                                                                                                                                                                                                                                                       USA
                  619-554-6312
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Pred. No. 6.4;
0; Mismatches 0; Indels
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Tatches 6; Conserv
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Best Local Similarity
6; Conserve
                                                                                                    US-08-060-833-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                               MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Logan, April C
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                ANTI-SENSE: NO FRAGMENT TYPE:
                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
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HYPOTHETICAL: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Cochrane, Charl APPLICANT: Revak, Susan D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: La Jolla
STATE: CA
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U
ZIP: 92037
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1 KLLLLK 6
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                              100.0%; ilarity 100.0%; Conservative 0,
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                                             Score 26;
Pred. No. 7
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Pred. No.
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                                 Mismatches
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                                                         Length 21;
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                                 Indels
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JS-08-735-171-1

Sequence 1, Application US/08735171 Patent No. 5741891 GENERAL INFORMATION:

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 908-524-2808
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                            NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                       APPLICANT: Cochrane, Charles G
APPLICANT: Revak, Susan D
TITLE OF INVENTION: PULMONARY SUI
TITLE OF INVENTION: POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Sampino, Keith
TITLE OF INVENTION: PULMONA
TITLE OF INVENTION: SOLUBIL
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                 STREET: 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
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TELEPHONE: 908-524-2641
                                      COUNTRY: U
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                                                                                 ADDRESSEE: Patent Counsel
STREET: 10666 No. 5789381th Torrey Pines Road, TPC 8
                                                                                                                                   ADDRESSEE:
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TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Dow, Kenneth J.
REGISTRATION NUMBER: 32,890
REFERENCE/DOCKET NUMBER: OR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/735,171
EILING DATE: 22-OCT-1996
CLASSIFICATION: 530
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                                                                                                                   The Scripps Research Institute, Office of
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Kasulanis, Charles F.
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                                                                                                                                                                               PULMONARY SURFACTANT PROTEIN AND RELATED
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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Best Local Similarity
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                                                                           TELEFAX: 732-524-2808
INFORMATION FOR SEQ ID NO:
                                                                                                                                         APPLICATION NUMBER: US/08/826
FILING DATE: 6-March-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Kenneth J.
REGISTRATION NUMBER: 32,890
REFERENCE/DOCKET NUMBER: ORT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Bornstein,
APPLICANT: Williams,
                                            SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 732-524-2641
                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Williams, N. Adeyinka
TITLE OF INVENTION: LYOPHILIZED PULMONARY SURFACTANT PEPTIDE COMPOSITIONS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Johnson & Johnson
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                 STATE: New
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 11-APCLASSIFICATION: 51
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linear
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US-08-826-261-1
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US-08-848-580-1
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APPLICANT: Cochrane, Charl
APPLICANT: Revak, Susan D
                                                                         TELEFAX: 619-784-9399
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/715,397
PRILING DATE: 14-JUN-1991
                                                                                                                                                                                                                    APPLICATION NUMBER: US 07 FILING DATE: 04-JAN-1989 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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PRIOR APPLICATION DATA:
US 08/488,123
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                                                           SEQUENCE CHARACTERISTICS
                                                                                                                     TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 0 FILING DATE: 06-JUN-1995
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nes 6; Conserva
                                                                                                                                                   REGISTRATION NUMBER:
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                 TOPOLOGY:
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 TYPE:
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                 linear
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peptide
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NO. 6013619th Torrey Pines Road, TPC-8
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Best Local Similarity
Whiches 6; Conserve
                                                      RESULT 12
PCT-US92-04537-7
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            Sequence 7, Application PC/TUS9204537 GENERAL INFORMATION:
APPLICANT: Cochrane, Charles G
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC -DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US 60/021,455
FILING DATE: 17-JUL-1996
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TITLE OF INVENTION: LIQUID PHASE PEPTIDE SYNTHESIS OF KL-4
TITLE OF INVENTION: PULMONARY SURFACTANT PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Dow, Kenneth J.
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Cochrane, Charles G
Revak, Susan D
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Maryanoff, C
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                                                                                                                                                                                                 100.0%; Score 26; DB 3; Length 21; 100.0%; Pred. No. 7.5;
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PCT-US92-04537-7
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Best Local Similarity 100.0%;
Matches 6; Conservative 0
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Patent No. 5739026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Garoff, Henrik
APPLICANT: Liljestrom, Peter
TITLE OF INVENTION: DNA Expression Systems Based on
TITLE OF INVENTION: Alphaviruses
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1001la
CITY: La Jolla
CMATE: California
ns
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FILING DATE: 14-UN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Relicument Application DATA:
APPLICATION NUMBER: PC
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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CLASSIFICATION:
                                                                                                                                                                                              STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 32,457
REFERENCE/DOCKET NUMBER: SCR1025P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
APPLICATION NUMBER: US/07/920,281C FILING DATE: 13-AUG-1992 CLASSIFICATION: 435
                                                                                                                                                                                    COUNTRY:
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Pred. No. 7.5;
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US-08-466-277-2
Sequence 2, Application US/08466277
Patent No. 6190666
GENERAL INFORMATION:
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Best Local Similarity

Matches 6; Conserv
US-08-466-277-2
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SEQUENCE CHARACTERISTICS:
LENGTH: 2431 amino acids
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NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 828-103P
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                                                                       TELEX: 248345
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2431 amino acids
TYPE: amino acid
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TELEFAX: 248345
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                                                                                                                                                                         APPLICATION NUMBER: 07/920,281
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 828-103P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
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                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,277
FILING DATE: 06-Jun-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 22040-0747

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: DNA Expression Systems Based
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Garoff, Henrik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                    TOPOLOGY: linear MOLECULE TYPE: protein
                 SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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100.0%; Pred. No.
tive 0; Mismatch
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STRANDEDNESS: single
TOPQLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PROSNOT20
CLONE: 1817518
US-09-088-549-1
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                                                                                                                              Query Match
Best Local Similarity
""tches 5; Conserve
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US-09-088-549-1
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Search completed: June 17, 2002, 12:42:04 Job time: 224 sec
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Best Local Similarity 100.
Matches 6; Conservative
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: CETTONE, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0530 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0572
TELEPHONE: 650-855-0572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: Fast-SEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: HILLMAN, JENNIFER L.
APPLICANT: CORLEY, NEIL C.
APPLICANT: PATTERSON, CHANDRA
TITLE OF INVENTION: HUMAN GLUTATHIONE PEROXIDASE-6
NUMBER OF SEQUENCES: 3
                                                                            1 KLLLIK 6
||:|||
178 KLILLK 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/088,549 FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KLLLLK 6
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83.3%;
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Result
No.
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Maximum
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OM protein - protein search, using sw model
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Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT:*
/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT:*
/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT:*
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/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1987.DAT:*
/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1987.DAT:*
/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1987.DAT:*
/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1997.DAT:*
/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
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                                                                                                                                                                                                                                                                        Length
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      AAW35155
AAW82853
AAB17419
AAW35152
AAW35152
AAW82847
AAW82850
AAW82850
AAW82850
AAW82850
AAW817416
AAB17416
                                                                                                                                                                                                                                                                        ID
                                                                                                                                                                                                                                                                                                                                      SUMMARIES
Leu/Lys diastereom Antipathogenic pep Antipathogenic pep Leu/Lys diastereom Leu/Lys diastereom Antipathogenic pep Antipathogenic pep
                                                                                                                                                                                                                                                                    Description
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C	30 85.7		•			85.	85.		85.	85.		85.		85.	85.		85.			•	85.		88.	88.	94.	94.	100.	100.	100.	100.	10	100.	100.
489 16	8				315 18	314	314	295	284	284		216	205	135	125	74	21	21	21	15	11	414	359	153	18	18	77	77	37	14	13	13	12
AAR/669/	AAR42176	ABG21008	AAU16931	ABG29956	AAW19946	AAE03235	AAB43933	AAW20723	AAR75494	AAR75397	AAB60324	AAB08846	ABG29958	AAY97766	AAU17004	ABG29957	AAB60066	AAU03187	AAW62968	AAW77384	AAB97447	AAE10702	AAW81359	AAY29393	AAR22830	AAR20977	AAW82859	AAW82858	AAW77378	AAW82854	AAB17482	AAW35231	48
Mouse MDM2 protein	e MDM2.	Novel human diagno	novel	Novel human diagno		Human gene 12 enco	an canc	H. pylori cytoplas	Human double minut	Human double minut	Helicobacter pylor	A human MDMIP-bind	Novel human diagno	I. scapularis Salp	Human novel secret	Novel human diagno	KL3 membrane activ	Membrane active sy	_	Lytic peptide with	_	GM3 s	Human alpha-2-3 si			7	Antipathogenic pep	thogenia	5	thogenio	Antipathogenic pep	pept	Antipathogenic pep

ALIGNMENTS

RESULT AAW35155

14-APR-1998 (first entry)

Leu/Lys diastereomer peptide [D]-L2,4,6-K3L5.

AAW35155,

AAW35155 standard; peptide;

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PAXRX FXX
                                                      Misc-difference
                                                                Misc-difference
                                                                                         Synthetic
(YEDA ) YEDA RES & DEV CO LTD
          22-FEB-1996;
                    20-FEB-1997;
                             28-AUG-1997
                                       WO9731019-A2
                                                                          Misc-difference
          96IL-0117223.
                    97WO-IL00066
                                                                         Location/Qualifiers
                                                       σ
                                                  /note=
                                                           /note= "D-form residue"
                                                                     /note= "D-form residue"
                                                  "D-form
                                                  residue"
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Leu/Lys diastereomer peptide; infection; therapy; excitatory neurotoxin; Honey bee venom; pardaxin; cytolytic activity; cancer; non-haemolytic; preservative; agricultural produce; bacterial cell lysis; agricultural pesticide; cell wall lysis.

continuity of an alpha-helical structure

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RESULT
AAW82853
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Best Local Similarity
"~+~hes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cc invention. The peptides of the invention have: (a) cytolytic activity on c pathogenic cells (pathogens and malignant cells not naturally present in cc pathogenic cells (pathogens and malignant cells not naturally present in cc concentration significantly higher than that at which they lyse concentration significantly higher than that at which they lyse concentrations (caused by bacteria, fungi, protozoa, mycoplasma or viruses) or cancer, in human and veterinary medicine. Also, they can be used as cc preservatives for food, cosmetics and agricultural produce, or as agricultural pesticides. The absence of haemolytic activity (associated with disturbance of alpha-helical structures) means that the peptides cc increased resistance to proteolytic degradation. Non-haemolytic, cytotoxic random copolymers of pardaxin, each has a specific spectrum of activity, allowing selection of agents for particular applications. Since resistance to them is unlikely to develop.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New non-haemolytic cytolytic agent useful in treating cancer infections - is a peptide comprising a moiety which disrupts
                                                                                                                                                                                                                                                                 Non-haemolytic; cytolytic; selective cytolytic activity; pathogen; cancer; infection; disinfectant; contact lens wetting solution; preservative; pesticide; fungicide; bactericide.
                                                                        Oren Z,
                                                                                                                                  20-FEB-1997;
                                                                                                                                                            19-FEB-1998;
                                                                                                                                                                                        27-AUG-1998
                                                                                                                                                                                                                W09837090-A1
                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                             Antipathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                 AAW82853 standard;
                                                                                                    (YEDA ) YEDA RES & DEV CO LTD
                                                                                                                                                                                                                                                                                                                                                            19-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide(s) having selective cytolytic activity - against pathogens and malignant cells, but no haemolytic activity, used for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a Leu/Lys diastereomer peptide of the invention have: (a) cytolytic activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
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                                             1998-594464/50.
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                                                                         Shai
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 40; 80pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                97WO-IL00066.
                                                                                                                                                           98WO-IL00081.
                                                                                                                                                                                                                                                                                                                             peptide
                                                                                                                                                                                                                                                                                                                                                                                                                peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
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Pred. No. 6.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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RESULT
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Best Local
                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                immunosuppressive; EPO; TPO; CTLA4; mimetic; II-1; TNF; antagonist; MMF; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB17419 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             breaker molety, or a peptide (or cyclic derivative of this) which (comprises L-amino acid residues and D-amino acid residues, has a net positive charge greater than 1 and has an amino acid sequence such that a corresponding amino acid sequence comprising only L-amino acid residues is not found in nature. The cytolytic agents may be used for treatment of cancer or for treatment of several diseases caused by pathogens, including bacterial, fungal, viral, mycoplasma and protozoan infections. They may be used in both human and veterinary medicine. They may also be used as disinfectants for destruction of microorganisms, i.e. in solutions for wetting contact lenses, as preservatives, e.g., in the cosmetic and food industries, as pesticides (e.g. fungicides or bactericides) or for preservation of agricultural products.
                                             WPI; 2000-350702/30.
                                                                           Feige U,
                                                                                                                                         23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                          25-OCT-1999;
                                                                                                                                                                                                                                                      WO200024782-A2
                                                                                                                                                                                                                                                                                                                                                                                                             Modified peptide; therapeutic agent;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Antipathogenic peptide sequence SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB17419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       specification describes a non-haemolytic, cytolytic agent, which is a peptide, a complex of bundled peptides, a mixture of peptides or a random peptide copolymer. The agent has a selective cytolytic activity on pathogenic cells. The agent is selected from a cyclic derivative of a peptide which has a net positive charge greater than 1, comprises L-amino acid residues and/or D-amino acid residues and comprises an alpha-helix
                                                                                                         (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                             autoimmune disease; cytostatic; antiasthmatic; thrombolytic; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present peptide is used to produce the agents of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 klilklik 8
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                                                                                                                                                                                                                                                                                                                   thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
8; Conserv
                                                                         Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 106;
                                                                                                                                                                                                                                                                                                                                                                                              disease;
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99US-0428082.
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                                                                             Cheetham
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Pred. No.
                                                                           Boone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                ID NO:523.
                                                                                                                                                                                                                                                                                                                                                                                                               fusion; Fc domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
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                                                                                                                                                                                                                                                                                                                                                                                                                cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                VEGF;
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0;

Novel composition of matter comprising an pharmacologically active peptides, useful

Fc domain and for treating

and

cancer and

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AAW35149
ID AAW3
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(X1)a-Fl-(X2)b, where: Fl = an Fc domain; X1 and X2 = are each

considered from -(L1)c-Pl-(L2)d-P2.

(L1)c-Pl-(L2)d-P2. (L3)e-P3, or -(L1)c-Pl-(L2)d-P2.

(L3)e-P3-(L4)f-P4

considered from -(L1)c-Pl-(L2)d-P2-(L3)e-P3-(L4)f-P4

considered from -(L1)c-Pl-(L2)d-P2-(L3)e-P3-(L4)f-P4

considered from -(L1)c-Pl-(L2)d-P2-(L3)e-P3-(L4)f-P4

considered from P3, or -(L1)c-Pl-(L2)d-P2-(L3)e-P3-(L4)f-P4

considered from P3, or -(L1)c-Pl-(L2)d-P2-(L3)e-P3-(L4)f-P4

considered from P4 = are each independently sequences of

considered from P4 = are each independently sequences of

considered from P5, or and P4 = are each independently

considered from P5, or and P5, or and P5, or autoimmune diseases.

considered from P5, or active from P5, or autoimmune diseases.

considered from P5, or actions and possibly placental transfer. AAA69443

considered from P5, or action, and possibly placental transfer. AAA69443

considered from P5, or action and possibly placental transfer. AAA69443

considered from P5, or action and possibly placental transfer. AAA69443

considered from P5, or action and possibly placental transfer. AAA69443

considered from P5, or action and possibly placental transfer. AAA69443

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considered from P5, or action and possibly placental transfer. AAA69443
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                  Leu/Lys diastereomer peptide; infection; therapy; excitatory neurotoxin; Honey bee venom; pardaxin; cytolytic activity; cancer; non-haemolytic; preservative; agricultural produce; bacterial cell lysis; agricultural pesticide; cell wall lysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW35149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW35149 standard;
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(YEDA ) YEDA RES & DEV CO LTD
                                  22-FEB-1996;
                                                                   20-FEB-1997;
                                                                                                                                         WO9731019-A2
                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                  Misc+difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leu/Lys diastereomer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-APR-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                     Misc#difference
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mes 8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KLLLKLLK 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 380;
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                                  96IL-0117223
                                                                   97WO-IL00066
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8
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12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide; 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide [D]-L3,4,8,10-K4L8.
                                                                                                                                                                                                                                                                                                                   "D-form
                                                                                                                                                                        "C-terminal amide
                                                                                                                                                                                                            "D-form residue"
                                                                                                                                                                                                                                             "D-form residue"
                                                                                                                                                                                                                                                                                "D-form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 35;
                                                                                                                                                                                                                                                                                residue"
                                                                                                                                                                                                                                                                                                                   residue"
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and linkers. Where (I)
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infections (caused by bacteria, fungi, protozoa, mycoplasma or viruses) or cancer, in human and veterinary medicine. Also, they can be used as preservatives for food, cosmetics and agricultural produce, or as agricultural pesticides. The absence of haemolytic activity (associated with disturbance of alpha helical structures) means that the peptides have few if any toxic effects, and those that include D-aa will have increased resistance to proteolytic degradation. Non-haemolytic, cytotoxic random copolymers of pardaxin, each has a specific spectrum of activity, allowing selection of agents for particular applications. Sinc these random copolymers induce total lysis of bacterial cell walls, resistance to them is unlikely to develop.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oren
                                                                                                                                                                                                                                                                              the body); but (b) no haemolytic activity, or such activity only at a concentration significantly higher than that at which they lyse pathogens. The peptides, their complexes and mixtures are used to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide(s) having selective cytolytic activity - against pathogens and malignant cells, but no haemolytic activity, used for treating
Sequence
                                                                                                                                                                                                                                                                                                                                                  pathogenic
                                                                                                                                                                                                                                                                                                                                                                       This sequence represents a Leu/Lys diastereomer peptide of the invention. The peptides of the invention have: (a) cytolytic activity
                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shai Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 39; 80pp;
                                                                                                                                                                                                                                                                                                                                                    cells
    12
                                                                                                                                                                                                                                                                                                                                                  (pathogens and malignant cells
                                                                                                                                                                                                                                                                                                                                                                                                                                        English.
                                                                                    each has a specific spectrum of or particular applications. Since
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Query Match
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Thes 8; Conserve
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                                   Misc-difference
                                                                                 Misc-difference
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                                                                                                                                                          Misc-difference
                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                   non-haemolytic; preservative; agricultural produce;
agricultural pesticide; cell wall lysis.
                                                                                                                                                                                                                                            Leu/Lys diastereomer peptide; infection; therapy; excitatory neurotoxin; Honey bee venom; pardaxin; cytolytic activity; cancer;
                                                                                                                                                                                                                                                                              Leu/Lys diastereomer peptide [D]-K1,5,9,12L2,6,7,11-K4L8
                                                                                                                                                                                                                                                                                                        14-APR-1998
                                                                                                                                                                                                                                                                                                                                AAW35152;
                                                                                                                                                                                                                                                                                                                                                        AAW35152
                                                                                                                                                                                                                                                      Leu/Lys diastereomer
                                                                                                                                                                                                                                                                                                                                                                                                                    1 KLLLKLLK 8
                                                                                                                                                                                                                                                                                                                                                                                 σ
                                                                                                                                                                                                                                                                                                                                                        standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                            /note=
                                                                                                                                                                    Location/Qualifiers
/note=
                     'note=
                                             note=
                                                                       /note=
                                                                                              note=
                                                                                                                     /note=
                                                                                                                                                                                                                                                                                                                                                       peptide;
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"D-form residue"
                      "D-form residue"
                                               "D-form
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                                                                                                                      "D-form
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Pred. No.
                                                                                                                                             residue"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                 bacterial
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В
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                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents a Leu/Lys diastereomer peptide of the invention. The peptides of the invention have: (a) cytolytic activity on the peptides of the invention have: (a) cytolytic activity on the peptides and malignant cells not naturally present in concentration significantly higher than that at which they lyse concentration significantly higher than that at which they lyse concentration significantly higher than that at which they lyse concentration significantly higher than that at which they lyse concentrations (caused by bacteria, fungi, protozoa, mycoplasma or viruses) concentratives for food, cosmetics and agricultural produce, or as concert in human and veterinary medicine. Also, they can be used as concentratives for food, cosmetics and agricultural produce, or as concentrative pesticides. The absence of haemolytic activity (associated have few if any toxic effects, and those that include D-aa will have concentrated resistance to proteolytic degradation. Non-haemolytic, concentrativity, allowing selection of agents for particular applications. Since these random copolymers of pardaxin, each has a specific spectrum of continuity, allowing selection of agents for particular applications. Since concentration to them is unlikely to develop.
                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                        Matches
                                                      Non-haemolytic; cytolytic; selective cytolytic activity; pathogen; cancer; infection; disinfectant; contact lens wetting solution; preservative; pesticide; fungicide; bactericide.
                                       Synthetic
                                                                                                                        Antipathogenic peptide.
                                                                                                                                                          19-MAY-1999
                                                                                                                                                                                        AAW82847;
                                                                                                                                                                                                                AAW82847 standard; peptide; 12
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide(s) having selective cytolytic activity - against pathogens and malignant cells, but no haemolytic activity, used for treating infections and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
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nes 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                             12
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                                                                                                                                                      (first entry)
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Pred. No. 2.6
); Mismatches
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                                                                                                                                                                                                                                                                                                                                                                         18;
                                                                                                                                                                                                                                                                                                                                              0;
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                                                                                                                                                                                                                                                                                                                                           0;
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WO9837090-A1

20-FEB-1997; 19-FEB-1998; 27-AUG-1998

98WO-IL00081.

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RESULT
AAW828
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Best Local S
Matches 8
                                                                                                                 Synthetic
                                                                                                                                                    Non-haemolytic; cytolytic; selective cytolytic activity; pathogen; cancer; infection; disinfectant; contact lens wetting solution;
                                                                                   WO9837090-A1
                                                                                                                                              preservative;
                                                                                                                                                                                                         Antipathogenic
                                                                                                                                                                                                                                                                                                                      850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a corresponding amino acid sequence comprising only 1-amino acid residues is not found in nature. The cytolytic agents may be used for treatment of several diseases caused by pathogens, including bacterial, fungal, viral, mycoplasma and protozoan infections. They may be used in both human and veterinary medicine. They may also be solutions for wetting contact lenses, as preservatives, e.g., in the cosmetic and food industries, as pesticides (e.g. fungicides or bactericides) or for preservation of agricultural products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present peptide is used to produce the agents of the invention. The specification describes a non-haemolytic, cytolytic agent, which is a peptide, a complex of bundled peptides, a mixture of peptides or a random peptide copolymer. The agent has a selective cytolytic activity on pathogenic cells. The agent is selected from a cyclic derivative of a peptide which has a net positive charge greater than 1, comprises L-amino acid residues and/or D-amino acid residues and comprises an alpha-helix (comprises L-amino acid residues and D-amino acid residues, has a net positive charge greater than 1 and has an amino acid sequence such that a contractive charge greater than 1 and has an amino acid sequence such that
                                                                                                                                                                                                                                        19-MAY-1999
                                                                                                                                                                                                                                                                      AAW82850
                                                                                                                                                                                                                                                                                                AAW82850 standard; peptide; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New non-haemolytic cytolytic agent useful in treating cancer infections - is a peptide comprising a moiety which disrupts continuity of an alpha-helical structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-594464/50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (YEDA ) YEDA RES & DEV CO LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 105; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                      (first entry)
                                                                                                                                              pesticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97WO-IL00066
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                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; s
100.0%; F
tive 0;
                                                                                                                                            fungicide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                         bactericide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                             19;/ Length
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the
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RESULT
AAW82856
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pathogenic cells. The agent is selected from a cyclic derivative of a peptide which has a net positive charge greater than 1, comprises L-amino acid residues and/or D-amino acid residues and comprises an alpha-helix breaker molety, or a peptide (or cyclic derivative of this) which (comprises L-amino acid residues and D-amino acid residues, has a net positive charge greater than 1 and has an amino acid sequence such that a corresponding amino acid sequence comprising only L-amino acid residues is not found in nature. The cytolytic agents may be used for treatment of cancer or for treatment of several diseases caused by pathogens, including bacterial, fungal, viral, mycoplasma and protozon infections. They may be used in both human and veterinary medicine. They may also be used a disinfectants for destruction of microorganisms, i.e. in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New non-haemolytic cytolytic agent useful in treating cancer infections - is a peptide comprising a moiety which disrupts continuity of an alpha-helical structure
                                                                                                                                                                                                                                                 Non-haemolytic; cytolytic; selective cytolytic activity; pathogen; cancer; infection; disinfectant; contact lens wetting solution; preservative; pesticide; fungicide; bactericide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
                 Oren Z,
                                                                                                                                                    27-AUG-1998
                                                                                                                                                                                    WO9837090-A1
                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                        Antipathogenic
                                                                                                                                                                                                                                                                                                                                                           19-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                           AAW82856 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cosmetic and food industries, as pesticides (e.g. fungicides or bactericides) or for preservation of agricultural products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present peptide is used to produce the agents of the invention. The specification describes a non-haemolytic, cytolytic agent, which is a peptide, a complex of bundled peptides, a mixture of peptides or a random peptide copolymer. The agent has a selective cytolytic activity on
                                                 (YEDA ) YEDA RES & DEV CO LTD
                                                                                    20-FEB-1997;
                                                                                                                    19-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                             AAW82856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   solutions for wetting contact lenses, as preservatives, e.g.,
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5 klllkllk 12
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                 Shai Y;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106; 126pp; English.
                                                                                    97WO-IL00066.
                                                                                                                    98WO-IL00081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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2.6;
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Best Local (
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               Feige U,
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The present peptide is used to produce the agents of the invention. The specification describes a non-haemolytic, cytolytic agent, which is a peptide, a complex of bundled peptides, a mixture of peptides or a random peptide copplymer. The agent has a selective cytolytic activity on pathogenic cells. The agent has a selective cytolytic activity on pathogenic cells. The agent is selected from a cyclic derivative of a peptide which has a net positive charge greater than 1, comprises L-amino acid residues and/or D-amino acid residues and comprises an alpha-helix breaker moiety, or a peptide (or cyclic derivative of this) which comprises L-amino acid residues and D-amino acid sequence such that a corresponding amino acid sequence comprising only L-amino acid residues is not found in nature. The cytolytic agents may be used for treatment of
cancer or for treatment of several diseases caused by pathogens, including bacterial, fungal, viral, mycoplasma and protozoan infection. They may also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 14; Page 106; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   continuity of an alpha-helical structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New non-haemolytic cytolytic agent useful in treating cancer or infections - is a peptide comprising a moiety which disrupts the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-594464/50
     infections. may also be
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1 KLLLKLLK 8
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5 klllkllk 12
                        8; Conserv
                        Conservative
                              100.0%;
                        0;
                              Score
Pred.
                        Mismatches
                               No.;
                              DB
2.6;
                                     19;
                        0
                                     Length 12
                         Indels
                        0;
                        Gaps
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Modified peptide; therapeutic agent; fusion; Fc domain, vecces autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; MMP; inhibitor; erythropoietin 4; tumour necrosis factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB17413 standard; Peptide; 12
(AMGE-) AMGEN INC
                                                               23-OCT-1998;
22-OCT-1999;
                                                                                                                                                            25-OCT-1999;
                                                                                                                                                                                                                        04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                     asthma; thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antipathogenic peptide sequence SEQ ID NO:517.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                  98US-0105371
99US-0428082
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                                                                                                                                                                                                                                                                                                                                                                                                                  pharmaceutical.
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antagonist;

Liu C,

Cheetham

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Boone

Claim

39; Page 378; 608pp; English.

pharmacologically

diseases

2000-350702/30.

composition of matter comprising an Fc domain and acologically active peptides, useful for treating of

cancer

and

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AAB17416
IID AABB
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AC AAB1
XX
AC AC AAB1
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AC AC AC AC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes composition of matter (I) comprising an CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each CC (L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 (CC where P1, P2, P3, and P4 = are each independently sequences of CC where P1, P2, P3, and P4 = are each independently sequences of CC independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently cC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive cc useful for treating cancer, asthma, thrombosis, or autoimmune diseases. CC The use of an Fc domain (rather than a Fab domain) can provide a longer CC half-life or incorporate functions such as Fc receptor binding, protein cc to AAA69526 and AAB16955 to AAB16003 represent nucleotide and amino acid xxx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                  Feige U,
                                                                                                                                                        23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                                  25-OCT-1999;
                                                                                                                                                                                                                                                                                           04-MAY-2000
                                                                                                   (AMGE-) AMGEN
                                                                                                                                                                                                                                                                                                                                              W0200024782-A2
                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 asthma; thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified peptide; therapeutic agent; fusion; Fc domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antipathogenic peptide sequence SEQ ID NO:520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB17416 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB17416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KLLLKLLK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
8; Conserv
                                                Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                   98US-0105371
99US-0428082
                                                                                                                                                                                                                               99WO-US25044
                                          Cheetham
                                                                                                                                                                                                                                                                                                                                                                                                                                                    lymphocyte antigen 4; tumour necrosis factor
lial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                          'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                          Boone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 35; [
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB
2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; cancer;
lvtic; VEGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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AAB17483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CC The present invention describes composition of matter (I) comprising an CC (X1)a-FI-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each CC (X1)a-FI-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each CC independently selected from -(L1)c-P1. (L1)c-P1-(L2)d-P2. (L4)f-P2 -(L3)e-P3-(L4)f-P4 (CC independently selected from -(L1)c-P1. (L2)d-P2-(L3)e-P3-(L4)f-P4 (CC where P1, P2, P3, and P4 = are each independently sequences of CC independently linkers; and a, b, c, d, e, and f = are each independently sequences of CC independently linkers; and a, b, c, d, e, and f = are each independently CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive CC be used for producing pharmaceutical compositions. The compositions are CC The use of an Fc domain (rather than a Fc receptor binding, protein CC a binding, complement fixation, and possibly placental transfer. AAA6943 CC sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 8; Conserv
         WPI; 2000-350702/30
                                          Feige U,
                                                                                                   23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                                                                Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; II-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                     (AMGE-) AMGEN INC.
                                                                                                                                              25-OCT-1999;
                                                                                                                                                                            04-MAY-2000
                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                     W0200024782-A2
                                                                                                                                                                                                                                                                                                                                                                         Antipathogenic peptide sequence SEQ
                                                                                                                                                                                                                                                                                                                                                                                                              31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB17483 standard; Peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB17483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KLLLKLLK 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39; Page 379; 608pp; English
                                     Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                99US-0428082
                                                                                                                98US-0105371
                                                                                                                                         99WO-US25044.
                                     Cheetham
                                                                                                                                                                                                                                                            Pharmaceutical Pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; S
100.0%; F
tive 0;
                                    J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 35;
Pred. No.
                                  Boone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                  TC;
                                                                                                                                                                                                                                                                                                                                                                           ID NO:587.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 12;
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RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  where [1], P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently 0 or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAAA6943 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                      autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CA4; minmetLic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoletin; thrombopoletin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     For domain, pharmacologically active peptides, and linkers, where (I) (X1)_A-F1-(X2)_b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-F1-(L1)c-F1-(L1)d-F2, (L1)c-F1-(L2)d-F2-(L3)e-F3-(L4)f-F4-(L1)c-F1-(L2)d-F2-(L3)e-F3-(L4)f-F4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating
Novel composition of matter comprising an Fc domain and
                                                                                                                        23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                      25-OCT-1999;
                                                                                                                                                                                                  04-MAY-2000
                                                                                                                                                                                                                                WO200024782-A2
                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                             asthma;
                                                                                                                                                                                                                                                                                                                                                                               Modified peptide; therapeutic agent; fusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                              31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB17485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB17485 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes composition of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                autoimmune
                              WPI; 2000-350702/30
                                                            Feige U,
                                                                                                                                                                                                                                                                                                                                                                                                               Antipathogenic peptide sequence SEQ ID NO:589.
                                                                                          (AMGE-) AMGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KLLLKLLK 8
||||||||
5 klllkllk 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
8; Conserv
                                                                                                                                                                                                                                                                                           thrombosis;
                                                            Liu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 401; 608pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                          c,
                                                                                                                      98US-0105371
99US-0428082
                                                                                                                                                                    99WO-US25044
                                                            Cheetham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 35; Pred. No.
                                                             Boone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                            TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .6;
                                                                                                                                                                                                                                                                                                                                                                                 Fc domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   matter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer and
                                                                                                                                                                                                                                                                                                                                                                                  cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Sequence

12

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cc independently selected from -(Li)c-Pi, -(Li)c-Pi-(L2)d-P2, (L3)e-P3, or -(Li)c-Pi-(L2)d-P2-(L3)e-P3-(L4)f-P4

cc where P1, P2, P3, and P4 = are each independently sequences of

cc pharmacologically active peptides; L1, L2, L3, and L4 = are each independently

cc independently linkers; and a, b, c, d, e, and f = are each independently

cc independently linkers; and a, b, c, d, e, and f = are each independently

cc or 1, provided that at least 1 of a and b is 1. The composition can

cc have cytostatic, antiasthmatic, thrombolytic and immunosuppressive

cc activities. DNAs, vectors and host cells from the present invention can

cc be used for producing pharmaceutical compositions. The compositions are

cc useful for treating cancer, asthma, thrombosis, or autoimmune diseases.

cc The use of an Fc domain (rather than a Fab domain) can provide a longer

cc half-life or incorporate functions such as Fc receptor binding, protein

cc A binding, complement fixation, and possibly placental transfer. AAA69443

cc to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid

sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pharmacologically active peptides, useful for treating cancer and autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fc domain, pharmacologically
(X1)a-F1-(X2)b, where: F1 =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention describes composition of matter (I) comprepharmacologically active peptides, and linkers. Where 2)b, where: F1 = an Fc domain; X1 and X2 = are each
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    608pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (I) comprising (ers. Where (I)
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AAW35231
ID
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Best Local Similarity
""" 8; Conserv
                                                                                                                          Misc-difference
                                                                                                                                                   Misc-difference
                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                           agricultural pesticide;
                                                                                                                                                                                                                                                                                         Diastereomer peptide; infection; therapy; excitatory neurotoxin; Honey bee venom; pardaxin; cytolytic activity; cancer; non-haemolytic; preservative; agricultural produce; bacterial ce
                                                                                                                                                                                                                                                                                                                                                Diastereomer
                                                                                                                                                                                                                                                                                                                                                                                                        AAW35231;
                                                                                                                                                                                                                                                                                                                                                                                                                                AAW35231 standard; peptide; 13 AA
 22-FEB-1996;
                           20-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                           14-APR-1998
                                                      28-AUG-1997
                                                                                 WO9731019-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 klllkllk 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KLLLKLLK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                              peptide [D]-L3,4,8,10-K4L8C
                                                                                                                                                                                                                                                                                                                                                                         (first entry)
96IL-0117223.
                           97WO-IL00066
                                                                                                          /note=
                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                /note=
                                                                                                                                                                                            /note=
                                                                                                                                      'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                             "D-form residue
                                                                                                                                                                  "D-form residue"
                                                                                                                                                                                             "D-form residue
                                                                                                                                      "D-form residue
                                                                                                                                                                                                                                                                             cell wall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                            lysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                          bacterial cell lysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents a diastereomer peptide of the invention. This consequence is used in a "bundle sequence", which is created by binding 5 copies of this sequence to peptide 23 (see AAW35149). The peptides of the invention have: (a) cytolytic activity on pathogenic cells (pathogens and malignant cells not naturally present in the body); but (b) no consequence of the invention have: (a) cytolytic activity on pathogens cells (pathogens and malignant cells not naturally present in the body); but (b) no consequence of the peptides of their complexes and mixtures are used to treat infections consequence of consequence of consequence of the peptides, their complexes and mixtures are used to treat infections consequence of in human and veterinary medicine. Also, they can be used as preservatives for food, cosmetics and agricultural produce, or as agricultural preservatives consequence of halpha-helical structures) means that the peptides have few if any toxic effects, and those that include D-aa will have increased conjumers of pardaxin, each has a specific spectrum of activity, colours selection of agents for particular applications. Since these condom copolymers induce total lysis of bacterial cell walls, resistance to them is unlikely to develop.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 8
                                                                                                                                                                                                                                           MMP; inhibitor; erythropoietin; thrombopoietin; interleukin i cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor vascular endothelial growth factor; matrix metalloproteinase;
                                            23-OCT-1998;
22-OCT-1999;
                                                                                                                                04-MAY-2000
                                                                                                                                                                WO200024782-A2
                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                              autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; mMMP; inhibitor; cytythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
            (AMGE-) AMGEN
                                                                                              25-OCT-1999;
                                                                                                                                                                                                                              asthma; thrombosis; pharmaceutical
                                                                                                                                                                                                                                                                                                                            Modified peptide; therapeutic agent; fusion; Fc
                                                                                                                                                                                                                                                                                                                                                                Antipathogenic peptide sequence SEQ ID NO:586.
                                                                                                                                                                                                                                                                                                                                                                                                       31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB17482 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide(s) having selective cytolytic activity - against pathogens and malignant cells, but no haemolytic activity, used for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oren
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8; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 AA;
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                                            98US-0105371.
99US-0428082.
                                                                                              99WO-US25044.
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                                                                                                                                                                                                                                                            factor;
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New non-haemolytic cytolytic agent useful in treating cancer infections - is a peptide comprising a moiety which disrupts

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RESULT
AAW82854
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CC (II)c-PI-(LZ)d-P2-(L3)e-P-3, or -(L1)c-PI-(LZ)d-P2-(L3)e-P3-(L4)f-P4 (L2)d-P2-(L3)e-P3-(L4)f-P4 (L2)d-P2-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3
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                                                        WPI; 1998-594464/50
                                                                                                   Oren
                                                                                                                                                                                                                                                                                                                                                                               Non-haemolytic; cytolytic; selective cytolytic activity; pathogen; cancer; infection; disinfectant; contact lens wetting solution; preservative; pesticide; fungicide; bactericide.
                                                                                                                                        (YEDA )
                                                                                                                                                                                 20-FEB-1997;
                                                                                                                                                                                                                      19-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                               Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                  CC pathogenic cells. The agent is selected from a cyclic derivative of a C pethode which has a net positive charge greater than 1 comprises L-amino CC acid residues and/or D-amino acid residues and comprises an alpha-helix CC breaker molety, or a peptide (or cyclic derivative of this) which CC comprises L-amino acid residues and D-amino acid residues, has a net CC comprises L-amino acid residues and D-amino acid residues, has a net CC comprise CC contributive charge greater than 1 and has an amino acid sequence such that CC corresponding amino acid sequence comprising only L-amino acid tresidues CC is not found in nature. The cytolytic agents may be used for treatment of CC cancer or for treatment of several diseases caused by pathogens, CC including bacterial, fungal, viral, mycoplasma and protozoan infections. CC They may be used in both human and veterinary medicine. They may also be CC used as disinfectants for destruction of microorganisms, i.e. in CC commetic and food industries, as preservatives, e.g., in the CC cosmetic and food industries, as pesticides (e.g. fungicides or CC bactericides) or for preservation of agricultural products.
                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present peptide is used to produce the agents of the invention. The specification describes a non-haemolytic, cytolytic agent, which is a peptide, a complex of bundled peptides, a mixture of peptides or a random peptide copolymer. The agent has a selective cytolytic activity on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 14; Page 106; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                 Sequence
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hypothetical prote
ABC transporter, A
probable serine/th
hypothetical prote
hypothetical prote
probable PPE prote
                                                                                                                                                                                            hypothetical protein - Trypanosoma brucei (fragment)
(;Species: Trypanosoma brucei
C;Species: Trypanosoma brucei
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Sep-1997
C;Accession: S27846
R;Woodward, R.; Carden, M.J.; Gull, K.
submitted to the EMBL Data Library, March 1992
A;Reference number: S27846
A;Accession: S27846
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S27846
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R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dods rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterbathey, L.; Weidman, J.; Smith, H.O.; Venter, J.C. Science 281, 375-388, 1998
                                                                                                                    A;Molecule type: mRNA
A;Residues: 1-302 <WOO>
A;Cross-references: EMBL:M87318; NID:g162176; PID:g162177
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C;Superfamily: unassigned ATP-binding cassette prote C;Superfamily: unassigned ATP-binding cassette homology <ABC>F;27-207/Domain: ATP-binding cassette homology <ABC>
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A;Residues: 1-238 <COL>
A;Cross-references: GB:AE001188; GB:AE000520; NID:g3322282;
A;Experimental source: strain Nichols
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A;Accession: E71375
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E71375
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Matches 7
Query Match 91. Best Local Similarity 87. Matches 7; Conservative
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55 KLVLKLLK 62
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1; Mismatches
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J.K.; Chidambaram, M.; Utterback,
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lactosylceramide alpha-2,3-sialytransferase (EC 2.4.99.9) - mouse C;Species: Mus musculus (house mouse) C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change I1 C;Accession: JE0364 R;Kono, M.; Takashima, S.; Liu, H.; Inoue, M.; Kojima, N.; Lee, Y. Biochem. Biophys. Res. Commun. 253, 170-175, 1998 A;Title: Molecular cloning and functional expression of a fifth-ty A;Reference number: JE0364; MUID:99092398
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JE0364
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A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A:Reference number: A97700; MUID:21442074; PMID:11557893
                                                                                                                                                                                                                                                                                                                                                                                       C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type:
A; Residues: 1-296
                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein RC0799 [imported] - Rickettsia conorii (strain Malish 7) C;Species: Rickettsia conorii (c:Species: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 30-Sep-2001 C;Accession: G97799
                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AE006914; PIDN:AAL03337.1; PID:g15619897; GSPDB:GN00173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 75.00
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                       Query Match
Best Local (
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                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:D14982; NID:g416237; PIDN:BAA03619.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic Acids Res. 21, 4816-4823, 1993
A;Title: Mapping of replication initiation site in A;Reference number: 542116; MUID:94051609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C:Species: Mycoplasma capricolum
C:Date: 07-Sep-1994 #sequence_revision 26-May-1995 #text_change 20-Jun-2000
C:Accession: S41121
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S42121
RNaseP C5 chain -
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                                                                                                                                                                                                                         294
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75.0%;
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75.08;
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Pred. No.
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Pred. No.
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64;
                                                         Kojima, N.; Lee, Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
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                                                                                      #text_change 11-May-2000
                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                       Length 296
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                   fifth-type alpha2,3-sialyltrar
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                                                       Hamamoto,
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                                                   T.; Tsuji
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A; Description:
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hypothetical protein UU580 [imported] - Ureaplasma urealyticum c;Species: Ureaplasma urealyticum c;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change C;Accession: H82873 R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Cher
                                         submitted to GenBank,
                                                                                                                                                                       RESULT
H82873
                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein
A; Molecule type: protein
A; Residues: 284-292, 'X', 294-296, 'R', 568-577; 751-753, 'L', 755-759; 765-776, 'T', 778-780; 8
A; Experimental source: erythrocyte
A; Mote: 885-His was also found
C; Superfamily: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase I; 1-phosphatodiesterase domain Y homology
Odiesterase domain Y homology
                                                                                                                                                                                                                                                                                                                                                                                                C;Keywords: phosphoric diester hydrolase
F;314-463/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain
F;543-663/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Experimental source: erythrocyte R;Waldo, G.L.; Morris, A.J.; Klapper, D.G.; Harden, T.K. Mol. Pharmacol. 40, 480-489, 1991
A;Title: Receptor- and G-protein-regulated 150-kDa avian phospholipase ished by immunoreactivity and peptide sequence.
A;Reference number: A61270; MUID:92017673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
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A;Residues: 210-216,'M',218-231;244-248;284-291;345-353,'S',355-360;453-461;661-679
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A: Residues: 1-1211 <WAL1>
A: Cross-references: GB:U49431.
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A;Reference number: S68251,
A;Accession: S68251
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Biochem. J. 316, 559-568, 1996
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-387 < KKON>
A;Cross-references: GB:Y15003
C;Superfamily: alpha-2,3-sialyltransferase
C;Keywords: glycosyltransferase
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                                                                                                                                                                                                                                                                                                                               Similarity 7; Conserv
Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, enBank, February 2000
The complete sequence of Ureaplasma urealyticum: Alternate views
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S72374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NID: 91223919; PIDN: AAC60011.1;
                                                                                                                                                                                                                                                                                                                      0;
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Pred. No.
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Pred. No.
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                                                                              #text_change 20-Aug-2000
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Alternate views of a

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A;Title: Genomic sequence comparison of two un A;Reference number: A71800; MUID:99120557 A;Reference number: A71800; MUID:99120557 A;Ression: G71932 A;Status: preliminary A;Molecule type: DNA A;Ressidues: 1-282 <ARN> A;Cross-references: GB:AE001477; GB:AE001439; A;Experimental source: strain J99 C;Genetics:
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A;Accession: H82873
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-166 <GLA>
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R; She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi Ngoc, H.P.; Redd arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001
A; Description: Sulfolobus solfataricus complete genome.
A; Reference number: A99139
A; Accession: F90392
                                                                                                                                                                                                          hypothetical protein jhp0431 - Helicobacter pylori (strain J99)
(;Species: Helicobacter pylori
A;Varlety: 'strain J99
C;Date: 12:Feb-1999 #sequence_revision 12-Feb-1999 #text_change 11-Jan-2000
C;Acccession: G71932
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.;
I'ves, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; V
Nature 397, 176-180, 1999
A; Gene: jhp043;
C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Genetics:
A;Gene: SSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein SSO2227 [imported] - Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001 C;Accession: F90392
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A;Experimental source: serovar 3; biovar 1
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A; Residues: 1-191 <KUR>
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Best Local S
Matches 6
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Best Local
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    Helicobacter
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75.0%;
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87.5%;
  hypothetical protein
                                                                           GB:AE001439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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Pred. No.
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Pred.
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58;
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67;
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                                                                           NID:g4154961; PIDN:AAD06012.1; PID:g41549
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                                                                                                                                                                                          pat!
                                    A; Molecule type: DNA
A; Residues: 1-433 < KUN>
                                                                                               A; Reference number: A; Accession: A69735
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                                                                         A; Status: preliminary; nucleic acid sequence
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A; Gene: PH0507
C; Superfamily: un
C; Keywords: ATP
F; 27-230/Domain:
                                                                                                                                                                                                                                                                                          M.; Ohfuku, Y.; Funahasnı, I.; Iuuun, ...
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophili
A;Reference number: A71000; MUID:98344137
                                                                                                                                                                                           A;Cross-references: GB:AP000002; NID:g3236129; A;Experimental source: strain OT3 A;Note: this accession replaces an interim acce C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                               R;Kawarabayasi, Y.; Sawada, M.;
M.; Ohfuku, Y.; Funahashi, T.;
                                                                                                                                                                                                                                                                                                                                                                                              C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 17-Mar-2000
C;Accession: F71163
                                                                                                                                                                                                                                                                                                                                                                                                                         probable oligopeptide transport ATP-binding protein AppF - Pyrococcus horikoshii
C; Species: Pyrococcus horikoshii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      망
                                                                                                                                                                                                                                                         A; Residues: 1-321 <KAW>
                                                                                                                                                                                                                                                                       A; Molecule type: DNA
                                                                                                                                                                                                                                                                                  A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                        Query Match
Best Local
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Best Local Similarity
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| 171 KIVLKLLK 178
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                             1 KLLLKLLK 8
KLILRLLK 62
                                                       6; Conserv
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                                                                                                                                 ATP-binding cassette
                                                          Conservative
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75.0%;
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75
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Tanaka, T.; Kudoh, Y.;
                                                        Score 30; DB Pred. No. 1.1e 2; Mismatches
                                                          2;
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Pred.
                                                                                                                                                                                                            interim accession
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                                                                                                                                 homology
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                                                    DB 2,
1.1e+02;
0;
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Yamazaki, J.;
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C. Bron. S. Broullet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997
A.; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galicch, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scand, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiquchi, J.; Sekowska, A.; Se akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida A.; Authors: Yoshikawa, H.; Danchin, A.
A.; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili A.; Reference number: A69580; MUID:98044033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phage PBSX terminase large chain xtmB - Bacillus subtilis C;Species: Bacillus subtilis C;Species: Bacillus subtilis C;Species: Bacillus subtilis C;Species: D5-Dec-1997 #sequence_revision O5-Dec-1997 #text_change 15-Oct-1999 C;Accession: A69735; I40415; S47115 C;Accession: A69735; I40415; S47115 R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Be: C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
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Cross-references:

source: strain

Devine,

K.M.; McConnell, D.J

GB:Z99110; GB:AL009126; NID:g2633472; PIDN:CAB13115.1; PID:e11832 ce: strain 168

not shown; translation

not

В

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A;Cross-references: EMBL:212020; NID:g35211; PIDN:CAA78055.1; PID:g35212 R.Zauberman, A.; Flusberg, D.; Haupt, Y.; Barak, Y.; Oren, M. Nucleic Acids Res. 23, 2584-2592, 1995
A.Title: A functional p53-responsive intronic promoter is contained within A; Reference number: S57338; MUID:95380270
A.Accession: S57338
A;Status: translation not shown
                                                                                                                                                                                                                                                             N;Contains: p53-binding protein mdm2, s
C;Species: Homo sapiens (man)
C;Date: 17-Mar-2000 #sequence_revision
C;Accession: S24354; S57338; G02026
A; Molecule
                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-491 <OLI>
                                                                                                                                                                                           A; Title: Amplification of a A; Reference number: S24354;
                                                                                                                                                                                                                              R;Oliner, J.D.; Kinzler, K.W.; Meltzer, P.S.; George, Nature 358, 80-83, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qy
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A; Residues: 1-489 < FAK>
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C; Accession: S15349
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A;Title: Genetic control of bacterial suicide: regu
A;Reference number: 140408; MUID:94364963
A;Accession: I40415
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-76 <RES>
                                                                                                                                                                          A; Accession: S24354
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N;Alternate names: mdm-2 oncogene;
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A;Gene: xtm
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Best Local Similarity 100.
7; Conservative
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100.0%; Pr
0;
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75.0%;
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Pred. No. 1.5e
2; Mismatches
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                                                                                                                                                                                                                                                                              17-Mar-2000
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1.5e+02;
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1.7e+02;
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C; Accession: T47638
R; Obermaier, B.; Ottenwae
submitted to the Protein
                                                                                                                          hypothetical protein T5N23.150 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000 C;Accession: T47638
                                                                                                                                                                                                    RESULT
T47638
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C; Superfamily: human p53-binding protein mdm2
C; Superfamily: human p53-binding protein mdm-2
C; Keywords: alternative splicing; oncogene; phosphoprotein
F;1-491/Product: p53-binding protein mdm-2 #status predicted <MAT1>
F;1-27,223-491/Product: p53-binding protein mdm-2, splice form A #sf
A; Molecule type: DNA
A; Residues: 1-727 <01
                                                     A; Reference number: A; Accession: T47638
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C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision
C;Accession: T39031
                                A; Status: preliminary
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A; Map position: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Devlin, K.; Churcher, C.M.; Barrell, B.G.; submitted to the EMBL Data Library, February
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A; Residues: 1-515 <DEV>
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A; Accession: T39031
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A;Cross-references: EMBL:U28935; NID:g904033; PIDN:AAA82237.1; PID:g904034
R;Lunec, J.
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A; Map position: 12q14.3-12q15
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A; Residues: 1-27, 223-491 <LUN>
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ce: splice form A
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87.5%;
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1.7e+02;
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                                                                                                         Mewes, H.W.; Lemcke,
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RNPA_MYCCA
XYMB_BACSU
MDM2_CANFA
MDM2_CANFA
MDM2_HUMAN
VD56_SCHPO
GGA3_HUMAN
VD56_STAAU
DPOL_NPVBM
CAPG_STAAU
SOML_TSTMU
SOML_STGGU
UBRL_KLULA
RL18_TRYBB
IPLL_YEAST
ASG2_BACSU
HE47_DROME
YPNP_BACSU
YC42_SYNY3
AAAT_RABIT
AAAX_BACSU
YC42_SYNY3
AAAT_RABIT
AAAX_BACSU
YC30_HELPY
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P56950 canis famil
P23804 mus musculu
P56951 eguus cabal
Q00987 homo sapien
Q10310 schizosacch
Q9nz52 homo sapien
P18131 autographa
P41712 bombyx mori
P39856 staphylococ
Q9i944 tetraodon m
P54863 sparus aura
P79894 sparus aura
Q9ygk7 sciaenops o
Q9pwg4 siganus gut
Q60014 kluyveromyc
P50885 trypanosoma
P3891 saccharomyc
Q34482 bacillus su
Q27268 drosophila
P54181 bacillus su
Q27268 staphylococ
P26899 bacillus su
Q47349 synechocyst
Q19192 mus musculu
Q45493 bacillus su
P51912 mus musculu
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6 bacillus su
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Query Match Best Local S Matches 7

Similarity 87. 7; Conservative

91.4%;

Score 32; DB Pred. No. 11; 1; Mismatches

1; 0;

Length 238; 0; Indels

0;

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OR DR DR DR DR VW SQ	4888888888888888888888888888888888888	R R R R R R R R R R R R R R R R R R R	YOS OCCOOC	
EMBL; AE00118; TIGR; TP0035; Interpro; IPR Interpro; IPR Interpro; IPR OFAm; PF00005 PROSITE; PS001 Hypothetical I Complete prott NP_BIND SEQUENCE 238	Science 281	SEQUENCE FR STRAIN-NICHC STRAIN-NICHC MEDLINE-983 Fraser C.M., Dodson R., C Sodergren E. Khalak H., H MCDOnald L., MCDOnald L., Hatch B., HC Yenter J.C., "Complete gespirochete."	RESULT 1 Y035_TREPA AC 083078; DT 16-0CT-2001 DT 16-0CT-2001 DT 16-0CT-2001 DT 17005ble met GN TP0035; GN Treponema po OC Bacteria; SF	00000000000000000000000000000000000000
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0 4 4 G 1 G	775-388(1998). PART OF AN ATP-DRIVEN 20035/TP0036 FOR A META TO THE TRANSPORT SYSTE AR LOCATION: Inner mem LOCATION: TOTHE ABC OT entry is copyright. SWISS Institute of Bio Bioinformatics Institut Swiss Institute of Bio Bioinformatics Institutions this statement is not this statement is not lices a license agreeme anires a license@isb-sib	fed= J., J., J., D., D., D.,	TANDARD; . 40, Crea: . 40, Last . 40, Last ransport s; um. haetales;	128 180 255 344 346 362 362 4434 470
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``	BLY RESPONSIBLE FOR ENERGY Sociated (Potential). TER FAMILY. TER FAMILY. TOUCHED through a collaboration ics and the EMBL outstation re are no restrictions on its as its content is in no way usage by and for commercial http://www.isb-sib.ch/announce/	G.G., Son J., Garland S., ith H.O.,		mycoplasma schizosacch elmeria ten methanococc saccharomyc archaeoglob escherichia hansenula w bacillus su methanococc bacillus su solanum tub

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KLLLKLLK 8 ||:||||| KLVLKLLK 62

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RRESULT 2
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OC BACTET
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XTMB_BACSU
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A Miyata M., Sano K.-I., Okada R., Fukumura T.,
RT "Mapping of replication initiation site in Mycoplasma capricolum
RT genome by two-dimensional gel-electrophoretic analysis.";
RT genome by two-dimensional gel-electrophoretic analysis.";
CC reprocessional gel-electrophoretic analysis.";
CC cleave other RNA substrates the removal of the 5'-leader sequence
CC cleave other RNA substrates such as 4.58 RNA. The protein
CC component plays an auxiliary but essential role in vivo by binding
CC to the 5'-leader sequence and broadening the substrate specificity
CC of the ribozyme (By similarity)
CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage of RNA, removing 5'-
CC --- CATALYTIC ACTIVITY: Endonucleolytic RNA component (M1 or rnpB) and a
                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local
                                                    01-FEB-1995
01-OCT-1996
16-OCT-2001
                            PBSX phage
                                                                                                                                XTMB_BACSU
P39786;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00825; Ribonuclease_P; 1.
PROSTTE; PS00648; RIBONUCLEASE_P; 1.
Hydrolase; Nuclease; Endonuclease; tRNA processing; RN
SEQUENCE 109 AA; 12900 MW; ACF520A0982C0D12 CRC64;
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HSSP; P25814;
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01-NOV-1995 (
16-OCT-2001
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01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ribonuclease P protein component (EC 3.1.26.5) (RNaseP protein)
(RNase P protein) (Protein C5).
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NCBI_TaxID=2095;
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SIMILARITY: BELONGS TO THE RNPA FAMILY.
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     (Rel. 31, Created)
(Rel. 34, Last sequence update)
(Rel. 40, Last annotation update)
terminase large subunit.
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75.0%;
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Pred. No. 8.2;
Pred. No. 8.2;
                                                                                                                                     PRT;
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RESULT 4
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Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2000 (Rel. : 30-MAY-2000 (Rel. : 01-MAR-2002 (Rel. : 01-MAR
                                                                                                                                   MEDLINE=20218866; PubMed=10754200; McFarlane S.T.,
                                                                                                                                                                                                                                                        Canis familiaris (Dog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
canine and equine homologues proto-oncogene.";
Cancer Lett. 152:9-13(2000).
                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
31-MAR-2000 (Rel. 41, Last annotation update)
Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (P53-binding protein Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein) (Cdm2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MDM2_CANFA
P56950;
                                                                                                                          Nasir L., Burr P.D.,
Argyle D.J.;
                                                                                            "Cloning, sequence
                                                                                                                                                                                                                                                     NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA packaging;
SEQUENCE 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SubtiList; BG11000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Z70177; CAA94059.1;
EMBL; Z34287; CAA84048.1;
EMBL; Z99110; CAB13115.1;
EMBL; Z99110; CAB13115.1;
PJR; S47115; S47115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Bacillus subtilis.
Bacteria; Firmicutes; Bacillus/Clostridium
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94364963; PubMed=8083174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=168
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39 KIVLKLLK 46
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les 6; Conserv
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                                                                 analysis and homologues of
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75.0%;
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o the EMBL/GenBank/DDBJ
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Pred.
                                                         expression of the cDNAs encoding the mouse double minute 2 (mdm2)
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                                                                                                                                        Gault E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    487
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51;
                                                                                                                                Thompson
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Canis.
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SEQUENCE FROM N.A. (ISOFORMS MDM2 MEDLINE=20065171; PubMed=10597303

(ISOFORMS MDM2 AND MDM2-ALPHA).

Query Match Best Local Similarity

Matches

Conservative

0;

Mismatches

0;

Indels

0,

0;

100.0%; 85.7%;

Score 30; Pred. No.

DB 57;

1;

Length 487

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VARSPLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                         PIAM; PF00279; MDM2; 1.

Pfam; PF00279; MDM2; 1.

Pfam; PF00641; zf-RanBP; 1.

SMART; SM00184; RING; 1.

PROSITE; PS01158; zF-RANBP2_1; 1.

PROSITE; PS50199; zF-RANBP2_2; 1.

PROSITE; PS50199; zF-RANBP2_2; 1.

PROSITE; PS50198; zF-RANBP2_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vitro and disrupts the p53-binding domain of mdm2 protein.";
Oncogene 18:7026-7033(1999).
-i- FUNCTION: INIBITS D53- AND P73-MEDIATED CELL CYCLE ARREST AND APOPTOSIS BY BINDING ITS TRANSCRIPTIONAL ACTIVATION DOMAIN.
FUNCTIONS AS AN UBIQUITIN LIGASE E3, IN THE PRESENCE OF E1 AND TOWARD P53 AND ITSELF. PERMITS THE NUCLEAR EXPORT OF P53 AND TARGETS IT FOR PROTEASOME-WEDIATED PROTEOLYSIS (BY SIMILARITY).
-i- COPACTOR: ZINC IS REQUIRED FOR UBIQUITIN LIGASE E3 ACTIVITY (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                       DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                             Zinc-finger;
                                                                                                                                                                                                                                                                                                                                                                                                     Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "A noyel exon within the mdm2 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Veldhoen N., Metcalfe S., Milner J.;
                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEIN (RB), EIA-ASSOCIATED PROTEIN P300 AND THE E2F1
TRANSCRIPTION FACTOR (BY SIMILARITY).
SUBCELLULAR LOCATION: NUCLEAR AND CYTOPLASMIC. EXPRESSED
PREDOMINANTLY IN THE NUCLEOPLASM (BY SIMILARITY).
ALTERNATIVE PRODUCTS: 2 ISOFORMS; MDM2 (SHOWN HERE) AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ITSELF (BY SIMILARITY).

SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
SIMILARITY: CONTAINS 1 RANBP2-TYPE ZINC FINGER.
SIMILARITY: BELONGS TO THE MDM2 / MDM4 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN: REGION I IS SUFFICIENT FOR BINDING P53 AND INHIBITING ITS G1 ARREST AND APOPTOSIS FUNCTIONS. IT ALSO BINDS P73 AND E2F1.
REGION II CONTAINS MOST OF A CENTRAL ACIDIC REGION REQUIRED FOR INTERACTION WITH RIBOSOMAL PROTEIN L5 AND A PUTATIVE C4-TYPE ZINC FINGER, THE RING FINGER DOMAIN WHICH COORDINATES TWO MOLECULES OF ZINC INTERACTS SPECIFICALLY WITH RNA WHETHER OR NOT ZINC IS RESENT AND MEDIATES THE HETERO-OLIGOMERIZATION WITH MDM4. IT IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALPHA; ARE PRODUCED BY ALTERNATIVE SPLICING. TISSUE SPECIFICITY: MDM2-ALPHA IS PRESENT IN TESTICULAR TISSUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY).

SUBUNIT: BINDS P53, P73, ARF(P14), RIBOSOMAL PROTEIN L5 AND SPECIFICALLY TO RNA. CAN INTERACTS ALSO WITH RETINOBLASTOMA PROTEIN 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALSO ESSENTIAL FOR ITS UBIQUITIN LIGASE E3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9UMT8; 1YCR
                                                                                                                                                                                                                                                                                                                                                                                                ; PS50089; ZF_RING_2; 1.
protein; Ligase; Ubiquitin conjugation; Oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; IPR003160; MDM2.
; IPR001876; Znf-Ra
; IPR001841; Znf_r
                                                                                                                                                                                                     190
210
210
242
243
                                                                                                                                                                                                                                                                                                                          Metal-binding; Alternative splicing.
19 108 REGION I.
179 185 NUCLEAR LOCALIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAF67833.1;
                                                                                                                            108
185
202
304
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215
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475
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     Œ,
                       (POTENTIAL).
MISSING (IN 1
G -> D (IN RE
QD -> HH (IN
                                                                                                                                              ASP/GLU-RICH
RANBP2-TYPE.
RING-TYPE.
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                                                                                                                         NUCLEOLAR LOCALIZATION SIGNAL
                                                                                                                                                                                                                                                         POLY-SER
                                                                                                                                                                                                                                                                             ARF BINDING.
                                                                                                                                                                                                                                                                                                  NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
  60CDB470A32A8E69 CRC64;
                                                 D (IN REF.
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domain of
                                                                           (IN ISOFORM MDM2-ALPHA)
                                                                                                                                                                                                  (ACIDIC)
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mdm2 protein.";
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TOWARD P53 A
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for
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RESULT
MDM2_M
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P23804: Q64330; Q61040;
Q1-NOV-1991 (Rel. 20, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
Q1-MAR-2002 (Rel. 41, Last annotation update)
Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (P53-1)
Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _MOUSE
                                                                                                                                                                                                                                   J. Biol.
[5]
                        MEDLINE=20079591; PubMed=10611322; Khosravi R., Maya R., Gottlieb T., Oren M., Shiloh Y., Shkedy "Rapid ATM-dependent phosphorylation of MDM2 precedes p53 accu in response to DNA damage."; Proc. Natl. Acad. Sci. U.S.A. 96:14973-14977(1999).
-!- FUNCTION: INHIBITS P53-AND P73-MEDIATED CELL CYCLE ARREST.
                                                                                                                                 MEDLINE-20180080; PubMed=10713175; Weber J.D., Kuo M.-L., Bothner B., DiGia Roussel M.F., Sherr C.J.; "Cooperative signals governing ARF-mdm2 localization of the complex."; Mol. Cell. Biol. 20:2517-2528(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genomic organization of Gene 175:209-213(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM MDM2-P90).
MEDLINE=91224107; PubMed=2026149;
Fakharzadeh S.S., Trusko S.P., George D.L.;
                                                                                                                                                                                                                                                             ultraviolet light.
                                                                                                                                                                                                                                                                                      Saucedo L.J., Myers C
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORMS MDM2-P90 MEDLINE-99175199; PubMed-10075719;
                                                                                                                                                                                                                                                                                                                                           "The organization and expr Genomics 33:352-357(1996).
                                                                                                                                                                                                                                                                                                                                                                      de Oca Luna R.M., Tabor A.D., Eberspaecher H., Worth L.L., Colman M.S., Finlay C.A., Lozano G
                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96299630;
de Oca Luna R.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jones S.N., Ansari-Lari M.A., Donehower L.A., Bradley A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97074674; PubMed=8917101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-129/SV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBO J. 10:1565-1569(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Tumorigenic potential associated with
that is amplified in a mouse tumor cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                     NUCLEOLAR LOCALIZATION SIGNAL. MEDLINE=20180080; PubMed=10713175;
                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=129/SV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090
                                                                                                       PHOSPHORYLATION BY ATM.
                                                                                                                                                                                                                                                                          "Multiple murine double minute gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33
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                                                                                                                                                                                                                                                 Chem.
AS
                                                                                                                                                                                                                                                274:8161-8168(1999).
 BINDING ITS TRANSCRIPTIONAL ACTIVATION \mbox{\sc Lan} ubiquitin ligase \mbox{\sc E3}, in the presence
                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=8660994;
                                                                                                                                                                                                                                                                                                                                                                                                                            (ISOFORM MDM2-P90)
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                           expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of the mouse double minute
                                                                                                                                                                                                                                                                                      .D., Perry M.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            iated with enhanced
tumor cell line.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hancock A.R., Jones W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Sciurognathi; Muridae,
                                                                                                                                                                                                                                                                                                                                                         of
                                                                                                                                                                                        DiGiammarino E.L.,
                                                                                                                                                                                                                                                                           2
                                                                                                                                                                                                                                                                                                                                                           the mdm2
                                                                                                                                                                                                                                                                                                                   AND
                                                                                                                                                                                                                                                                           (MDM2)
                                                                                                                                                               interaction
                                                                                                                                                                                                                                                                                                                   MDM2-P76)
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                                                                                                                                                                                          Kriwacki R.W.,
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                                                                                                                                                                                                                                                                            are induced
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  AND
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Pfam; PF02279; MDM2; 1.
Pfam; PF00641; zf-RanBP; 1.
SMART; SM00184; RING; 1.
PROSITE; PS01358; zF_RANBP2_1; 1.
PROSITE; PS50199; zF_RANBP2_2; 1.
PROSITE; PS00518; zF_RING_1; FALS
PROSITE; PS50089; ZF_RING_2; 1.
                                                                                                                                                                                                                                                                             EMBL; X58876;
EMBL; U47944;
EMBL; U47935;
EMBL; U47936;
EMBL; U47936;
EMBL; U47938;
EMBL; U47939;
EMBL; U47939;
EMBL; U47940;
EMBL; U47941;
EMBL; U47941;
EMBL; U47941;
EMBL; U47943;
EMBL; U47943;
                                                                                                                                                    InterPro; IPR001841;
                                                                                                                                                                        InterPro; IPR003160; MDM2.
InterPro; IPR001876; Znf-F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institumodified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOWARD P53 AND ITSELF. PERMITS THE NUCLEAR EXPORT OF P53 AND TARGETS IT FOR PROTEASOME-MEDIATED PROTEOLYSIS.

-!- COFACTOR: ZINC IS REQUIRED FOR UBIQUITIN LICASE E3 ACTIVITY. SUBUNIT: BINDS P53, P73, ARF(P14), RIBOSOMAL PROTEIN L5 AND SPECIFICALLY TO RNA. CAN INTERACTS ALSO WITH RETINOBLASTOMA PROTEIN (RB), E1A-ASSOCIATED PROTEIN P300 AND THE E2F1

TRANSCRIPTION FACTOR. NUCLEAR AND CYTOPLASMIC. EXPRESSED PREDOMINANTLY IN THE NUCLEOPLASM. INTERACTION WITH ARF(P14) RESULTS IN THE LOCALIZATION OF BOTH PROTEINS TO THE NUCLEOLUS. THE NUCLEOLAR LOCALIZATION SIGNALS IN BOTH ARF(P14) AND MDM2 MAY BE DEPARTMENT.
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DISEASE: THE G
CELL LINE.
SIMILARITY: CC
SIMILARITY: CC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN: REGION I IS SUFFICIENT FOR BINDING P53 AND INHIBITING ITS G1 ARREST AND APOPTOSIS FUNCTIONS. IT ALSO BINDS P73 AND E2F1. REGION II CONTAINS MOST OF A CENTRAL ACIDIC REGION REQUIRED FOR INTERACTION WITH RIBOSOMAL PROTEIN L5 AND A PUTATIVE C4 TYPE ZINC FINGER. THE RING FINGER DOMAIN WHICH COORDINATES TWO MOLECULES OF PRESENT AND MEDIATES THE HETERO-OLIGOMERIZATION WITH MDM4. IT IS PRESENT AND MEDIATES THE HETERO-OLIGOMERIZATION WITH MDM4. IT IS
                                                                                                                                                                                                                MGI:96952; Mdm2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              European Bioinformatics Institute.
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INDUCTION: BY UV LIGHT.

INDUCTION: BY UV LIGHT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is not removed. Usage by and for commercial agreement (See http://www.isb-sib.ch/announce/
                        FALSE_NEG
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SIMILARITY).

SIMILARITY DO RNA. CAN INTERACTS ALSO WITH RETINOBLASTOMA PROTEIN L5 AND SPECIFICALLY TO RNA. CAN INTERACTS ALSO WITH RETINOBLASTOMA PROTEIN (RB). E1A-ASSOCIATED PROTEIN P300 AND THE E2F1

TRANSCRIPTION FACTOR (BY SIMILARITY).

-1- SUBCELLULAR LOCATION: NUCLEAR AND CYTOPLASMIC. EXPRESSED PREDMINANTLY IN THE NUCLEOPLASM (BY SIMILARITY).

-1- DOMAIN: REGION I IS SUFFICIENT FOR BINDING P33 AND INHIBITING ITS G1 ARREST AND APOPTOSIS FUNCTIONS. IT ALSO BINDS P73 AND E2F1.

REGION II CONTAINS MOST OF A CENTRAL ACIDIC REGION REQUIRED FOR INTERACTION WITH RIBOSOMAL PROTEIN L5 AND A DYTARIVE C4-TYPE ZINC FINGER. THE RING FINGER DOMAIN WHICH COORDINATES TWO MOLECULES OF ZINC INTERACTS SPECIFICALLY WITH RNA WHETHER OR NOT ZINC IS PRESENT AND MEDIATES THE HETERO-OLIGOMERIZATION WITH MDM4. IT IS
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Best Local
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-I- FUNCTION: INHIBITS P53- AND P73-MEDIATED CELL CYCLE ARREST AND APOPTOSIS BY BINDING ITS TRANSCRIPTIONAL ACTIVATION DOMAIN.
FUNCTIONS AS AN UBIQUITIN LIGASE E3, IN THE PRESENCE OF E1 AND TOWARD P53 AND ITSELF. PERMITS THE NUCLEAR EXPORT OF P53 AND TARGETS IT FOR PROTEASOME-MEDIATED PROTEOLYSIS (BY SIMILARITY).

-I- COPACTOR: INC IS REQUIRED FOR UBIQUITIN LIGASE E3 ACTIVITY (BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (P53-binding Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein) (Edm2).
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CONFLICT
CONFLICT
SEQUENCE
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(Rel. 39, Last seq
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D., McFarlane S.T.,
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RING-TYPE.
NUCLEOLAR LOCALIZATION SIGNAL
(POTENTIAL).
S -> T (IN REF. 1).
D -> H (IN REF. 1).
S -> T (IN REF. 3).
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Pred. No.
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ARF BINDING.
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NUCLEAR LOCALIZATION
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-> T (IN REF. 3).
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Zinc; Zinc-finger;
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Best I
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SMART; SM00184; RING; 1.
PROSITE; PS01358; ZF_RANBP2_1; 1
PROSITE; PS50199; ZF_RANBP2_2; 1
PROSITE; PS50189; ZF_RING_1; FAL
PROSITE; PS50089; ZF_RING_2; 1.
Nuclear protein; Ligase; Ubiquit
Vogelstein B.;
"Amplification
sarcomas.";
                                                                                                                                                          MDM2_HUMAN
Q00987; Q13
Q9UMT8;
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ZN_FING
ZN_FING
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01-APR-1993 (Rel. 25, Last sequence upda
01-MAR-2002 (Rel. 41, Last annotation up
Ubiquitin-protein ligase E3 Mdm2 (EC 6.3
Mdm2) (Oncoprotein Mdm2) (Double minute
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InterPro;
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Mammalia;
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DOMAIN
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                           Oliner J.D.,
                                   SEQUENCE FROM N.A. MEDLINE-92310576;
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SIMILARITY: CONTAINS 1 RANBP2-TYPE ZI
SIMILARITY: CONTAINS 1 RANBP2-TYPE
SIMILARITY: BELONGS TO THE MDM2 / w
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LF (BY SIMILARITY)
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IPR001876; Znf-F
IPR001841; Znf_r
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                        A. (ISOFORM MDM2).
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zler K.W., Meltzer
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Primates;
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Pred. No. 58;
0; Mismatches
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RANBP2-TYPE.
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NUCLEOLAR LOCALIZATION SIGNAL
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Catarrhini;
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C 6.3.2.-) (P53-
nute 2 protein)
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i; Hominidae; Homo.
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Q13300; Q13301; Q9UGI3;
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                         George D.L.,
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and p53."
J. Biol.
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                                                                                                                                                                                                                                                                                                                                                  Cancer
[8]
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Zauberman A., Flusberg D., Haupt Y., E
"A functional p53-responsive intronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liang H., Atkins H., Abdel-Fattah R., Suaeyun R., "Genomic Organisation of the Human MIM2 Oncogene its Alternatively Spliced mRNA's.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ dat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   veldhoen N., Metcalfe S., Milner J.;
"A novel exon within the mdm2 gene modulates translation initiation
vitro and disrupts the p53-binding domain of mdm2 protein.";
oncogene 18:7026-7033(1999).
                                          MEDLINE=20187618; PubMed=10722742; Fang S., Jensen J.P., Ludwig R.L., Vousden "Mdm2 is a RING finger-dependent ubiquitin
                                                                                                  "Activity of MDM2, a ubiquit dependent on the RING finger Oncogene 19:1473-1476(2000).
                                                                                                                                                                                             MUTAGENESIS OF CYS-46
MEDLINE~98111004; Pub
Honda R., Tanaka H.,
"Oncoprotein MDM2 is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sigalas I., Calvert A.H., Anderson J.J., Neal D.E., | "Alternatively spliced mdm2 transcripts with loss of domain sequences: transforming ability and frequent
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[2]
                                                                                                                                    MEDLINE=20190101;
Honda R., Yasuda F
                                                                                                                                                                                    FEBS Lett.
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                                                                                                                                                                                                                                                                                                                                                                    Landers J.E., Cassel S.L., George D.L.;
"Translational enhancement of mdm2 oncogene cells containing a stabilized wild-type p53
                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97413643; PubMed=9270029;
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                      Chem.
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CYS-441 AND CYS-478
                     275:8945-8951(2000).
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Science
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sharp D.A., Kratowicz S.A., Sank M.J., "Stabilization of the MDM2 oncoprotein structurally related MDMX protein.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in response to DN Proc. Natl. Acad.
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Khosravi R., Maya R., Gottlieb T., Oren
"Rapid AUM-dependent phosphorylation of
in response to DNA damage.";
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Science 274:948-953(1996).
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"Structure of the MDM2 oncoprotein bound
"Structure of Annain.";
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MEDLINE=97081050; PubMed=8875929;
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DISEASE: SEEMS TO BE AMPLIFIED IN CERTAIN TUMORS (INCLUDI DISEASE: SEEMS TO BE AMPLIFIED IN CERTAIN TUMORS (INCLUDI TISSUE SARCOMAS, OSTEOSARCOMAS AND GLIOMAS). A HIGHER FRE SPLICE VARIANTS LACKING P53 BINDING DOMAIN SEQUENCES WAS LATE-STACE AND HIGH-GRADE OVARIAN AND BLADDER CARCINOMAS. THE SPLICE VARIANTS SHOW LOSS OF P53 BINDING.

THE SPLICE VARIANTS SHOW LOSS OF P53 BINDING.

MISCELLANBOUS: MDM2 RING FINGER MUTATIONS THAT FAILED TO UBIQUITINATE P53 IN VITRO DID NOT TARGET P53 FOR DEGRADAT
                                                                                                                                                                                                                                                                                                                                                                      ALTERNATIVE PRODUCTS: 8 ISOFORMS; MDM2 AL, MDM2-B, MDM2-C, MDM2-D, MDM2-E AND ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: UBIQUITOUS. ISOFORM ARE OBSERVED IN A RANGE OF HUMAN CANCER
                                                                                                                                                                                                                          DOMAIN: REGION I IS SUFFICIENT FOR BINDING P53 AND INHIBITING ITS G1 ARREST AND APOPTOSIS FUNCTIONS. IT ALSO BINDS P73 AND E2F1.

REGION II CONTAINS MOST OF A CENTRAL ACIDIC REGION REQUIRED FOR INTERACTION WITH RIBOSOMAL PROTEIN L5 AND A PUTATIVE C4-TYPE ZINC FINGER. THE RING FINGER DOMAIN WHICH COORDINATES TWO MOLECULES OF ZINC INTERACTS SPECIFICALLY WITH METHER OR NOT ZINC IS PRESENT AND MEDIATES THE HETERO-OLIGOMERIZATION WITH MINK. IT IS SPECIFICALLY WITH METHER OR NOT ZINC IS PRESENT AND MEDIATES THE UBIQUITIN LIGASE E3 ACTIVITY TOWARD P53 AND SESSENTIAL FOR ITS UBIQUITIN LIGASE E3 ACTIVITY TOWARD P53 AND MEDIATES THE METHER OF METHER OR NOT ZINC IS PRESENT AND MEDIATES THE METHERO-OLIGOMERIZATION WITH MINK.
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                                                                                                                           IN CERTAIN TUMORS (INCLUDING SOFT AND GLIOWAS). A HIGHER PREQUENCY OF FOMAIN SEQUENCES WAS FOUND IN
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InterPro; iPR001876; Znf_ranBP.
InterPro; iPR001841; Znf_ring.
InterPro; iPR001841; 1.
InterPro; iPR001841; 2f_RanBP; 1.
InterPro; iPR001858; Zf_RanBP; 1.
InterPro; iPR001858; Zf_RanBP; 1.
InterPro; iPR001858; Zf_RanBP; 1.
InterPro; iPR00186; Zf_RanBP; 2.
InterPro; iPR00186; Zf_RanBP; 1.
InterPro; iPR00186; Zf_RanBP; 2.
InterPro; iPR00186; Zf_RanBP; 1.
InterPro; iPR00186; Zf_RanBP; 2.
InterPro; iPR0018
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EMBL; Z12020; CAA78055.1; --
EMBL; U33199; AAA75514.1; --
EMBL; U33200; AAA75515.1; --
EMBL; U33201; AAA75516.1; --
EMBL; U33202; AAA75517.1; --
EMBL; U33203; AAA75518.1; --
EMBL; U33203; AAA05518.1; --
EMBL; U32835; AAA82237.1; --
EMBL; U28935; AAA82237.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                   Ol-OCT-1996 (Rel. 34, Created)
Ol-OCT-1996 (Rel. 34, Last sequence up
Ol-OCT-1996 (Rel. 34, Last annotation
Hypothetical 59.0 kDa protein C6C3.06
SPAC6C3.06.
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the Euro
                      use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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DOMAIN 19
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                                                                                                                                                                                                                                                                                                                                                               Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YD56.
                                                                                                                                                                                                  Devlin K., Churcher C.M., Barrell B.G., Rajandream M.A., Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
                                                                                                                        the European Bioinformatics Institute.
                                                                                                                                                 between
                                                                                                                                                                                                                                                      STRAIN=972;
                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                             Schizosaccharomyces
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1YCR; 19-NOV-97
164785; -.
                                                                                                                                             SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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CAA93619.1;
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                                                                                                                                                                        Nagase T., Seki N., Tanaka A., Ishikawa K.-I., Nomura N.;

"Prediction of the coding sequences of unidentified human gene
The coding sequences of 40 new genes (KIAAO121-KIAAO160) deduc
Tanalysis of cDNA clones from human cell line KG-1.";

DNA Res. 2:167-174(1995).

C -!- FUNCTION: MAY PLAY A ROLE IN THE REGULATION OF MEMBRANE TR
THROUGH THE TRANS-GOLGI NETWORK.

C -!- SUBJUNIT: BINDS TO ARF1.

C -!- SUBJUNITE BINDS TO ARF1.

C -!- SUBJUNITE BINDS TO ARF1.

C -!- ALITERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE)
SHORT FORM; ARE PRODUCTS: 2 SISOFORMS; PLICING.

C -!- TISSUE SPECIFICITY: UBJUNITOUSLY EXPRESSED.

C -!- SIMILARITY: CONTAINS 1 VHS DOMAIN.
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADP-ribosylation factor binding protein GGA3
                                                      modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dell'Angelica E.C., Puertollano R., Mullins C., Agu Vargas J.D., Hartnell L.M., Bonifacino J.S., "GGAs: a family of ADP ribosylation factor-binding adaptors and associated with the Golgi complex.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein. SEQUENCE 515 AA;
                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI
                                                                                                                                                                                                                                                                                                                                                                                       TISSUE Bone marrow; mEDLINE 96127530; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Boman A.L., Zhang C.-J., Zhu X., Kahn R.A.;
"A family of ADP-ribosylation factor effectors that can alter transport through the trans-Golgi.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Heart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ear-containing, ARF-binding protein GGA3 OR KIAA0154.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (SHORT ISOFORM).
MEDLINE=20214818; PubMed=10749927;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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AF219138;
AF190864;
AF219139;
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AAF42848.1;
AAF05709.1;
AAF42849.1;
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Best Local :
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P18131;
01-NOV-1990
01-NOV-1995
15-DEC-1998
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                                            the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                     MEDLINE-89073763; PubMed=3059678; Tomalski M.D., Wu J.G., Miller L.K.; "The location, sequence, transcription, baculovirus DNA polymerase gene."; Virology 167:591-600(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
EMBL; M20744;
EMBL; L22858;
                                                                                                                                                                                                 "The complete DNA sequence of Autographa opolyhedrosis virus.";
Virology 202:586-605(1994).
-i- CATALYTIC ACTIVITY: N deoxynucleoside
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Viruses; dsDNA viruses,
Nucleopolyhedrovirus.
NCBI_TaxID=46015;
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InterPro; IPR001121; G_adapt_C.
InterPro; IPR002014; HRS.
                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                            MEDLINE-94303173; PubMed-8030224;
Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., I
"The complete DNA sequence of Autographa californica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD003686; HRS; 1.
ProDom; PD021457; G_adapt_C;
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                                                                                                                                                                     -!- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY.
                                                                                                                                                                                                                                                                                              STRAIN=C6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Autographa californica nuclear polyhedrosis virus (AcMNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
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(Rel. 32, Last sequence update)
(Rel. 37, Last annotation update)
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MISSING (IN SHORT ISOFORM).
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DPOL_NPVBM
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DPOL_NPVBM SIGNAL....

P41712; 092430;
01-NOV-1995 (Rel. 32, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
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MEDILINE-95133178; PubMed=7831799;
Chaeychomsri S., Ikeda M., Kobayashi M.;
Nucleotide sequence and transcriptional analysis of the DNA
polymerase gene of Bombyx mori nuclear polyhedrosis virus.";
Virology 206:435-447(1995).
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Pfam; PF001136; DNA_pol_B; 1.
Pfam; PF031104; DNA_pol_B_exo; 1.
PRINTS; PR00106; DNAPOLB.
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              PROSITE; PS00116; DNA POLYMERASE_B; 1.
Transferase; DNA-directed DNA polymerase;
DNA-binding; Early protein.
                                                                                                                                                                                                        EMBL; D16231; BAA03756.1; -. EMBL; L33180; AAC63738.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY
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                                                                                       SMART; SM00486; POLBC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Sequence analysis of the genome of Bombyx mori
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                                                                                                                                                                                                                                                                    "Sequence analysis and molecular characterization of for the biosynthesis of type 1 capsular polysaccharic Staphylococcus aureus.", Bacteriol. 176.7005-7016(1994).

-I- FUNCTION: REQUIRED FOR THE BIOSYNTHESIS OF TYPE 1
                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus aureus.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
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                                                                           Transferase; SEQUENCE 1
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InterPro; IPR001451; Hexapep_transf.
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SIMILARITY: BELONGS TO THE CYSE/LACA/LDXA/NODL FAMILY OF
ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
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A -> S (IN REF. 1).
H -> Y (IN REF. 1).
H -> Y (IN REF. 1).
Y -> I (IN REF. 1).
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Pred. No.
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Pred. No.
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01-OCT-1996 (Rel. 34, Last sequence update)
15-UU-1999 (Rel. 38, Last annotation update)
Somatolactin 1 precursor (SL).
Sparus aurata (Gilthead sea bream).
                                                                                                                                                                                                                                                                                                      SOM1_SPAAU
P54863;
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01-MAR-2002 (Rel. 41, Created)

01-MAR-2002 (Rel. 41, Last sequence update)

01-MAR-2002 (Rel. 41, Last annotation updat
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Tetraodon miurus (Congo puffer).
Eukaryota, Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoide; Sparidae; Sparus.
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-!- SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning and sequencing of Tetraodon miurus somatolactin."; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE FROM N.A
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    -!- SUBCELLULAR LOCATION: Secreted

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Tetraodontidae; Tetraodon.
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Euteleostei; Neoteleostei;
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01-MAR-2002
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                                                                     Somatolactin 2 precursor (SL).
Sparus aurata (Gilthead sea bream).
Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Acanthomorpha; Acanthopterygii; Percomor
Sparus.
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            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                       SEQUENCE FROM N.A.
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HSSP; P01246; 1BST.
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-!- SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
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-!- SUBCELLULAR LOCATION: Secreted.
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Pred. No. 45;
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Euteleostei; Neoteleostei;
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O99wf6 mus musculu
O99wf9 mus musculu
O910f3 mus musculu
O910f3 epiphyas po
O910f6 meleagris g
O96ds1 homo sapien
O96ds1 homo sapien
O96ds1 homo sapien
O96ds1 homo sapien
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Q9jim7 mus musculu	Q9h952 homo sapien	homo	homo	Q9jiq6 mus musculu	Q9nru3 homo sapien	Q91xk7 mus musculu	Q95kn5 canis famil	Q9gmz6 canis famil	Q91dc5 oryza sativ	~	Q9pvl2 gallus gall		Q9z1z4 helicobacte	homo	Q961k7 homo sapien	5 ory	Q96ds4 homo sapien	Q97w19 sulfolobus	S	Q950q3 spizellomyc	Q96ds0 homo sapien	Q9dbl5 mus musculu	Q95wz4 ixodes scap	Q9h4c3 homo sapien	borr	Q9rzz6 borrelia bu	Q9s047 borrelia bu	Q9s089 borrelia bu

ALIGNMENTS

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Q26784;
Q1-NOV-1996 (TrEMBLrel. 0
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NON_TER
SEQUENCE
Q9IZC1;
01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                             Trypanosoma brucei.
Eukaryota; Euglenozoa; Kinetoplastida;
NCBI_TaxID=5691;
                                                                                                                                                                                                   MEDLINE-95140053; PubMed-7838181;
Woodward R., Carden M.J., Gull K.;
Woodward R., Carden M.J., Gull K.;
Molecular characterisation of a novel, repetitive protein of the paraflagellar rod in Trypanosoma brucet.";
Mol. Biochem. Parasitol. 67:31-39(1994).
EMBL; M87318; AAC37211.1; ...
                                         Q9IZC1
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                                                                                                                1 KLLLKLLK 8
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KLLLKVLK 28
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                                         PRELIMINARY;
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87.5%;
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Q948F3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases. EMBL; Y18023; CAC79655.1; -. SEQUENCE 194 AA; 22205 MW; E68780E30BFE84EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF237881; AAF63741.1; -...
InterPro; IPR002021; Paramyx_ncap.
Pfam; PF00973; Paramyx_ncap; 1.
SEQUENCE 542 AA; 60717 MW; F05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Renshaw R.W., Glaser A.L., Van Campen H., Weiland F., Dubovi E.J., "Identification and phylogenetic comparison of salem virus, a novel paramyxovirus of horses.", Virology 270.417-429(2000).
Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID-4530;
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01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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                                                                                                          PUTATIVE RIBONUCLEOTIDE OSJNBA0049012.22.
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01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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CR; TISSUE-BRAIN;
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Rodentia;
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87.5%;
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19, Last sequence update)
19, Last annotation update)
REDUCTASE (FRAGMENT).
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Pred. No. 1.6e
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Pred. No. 1.1e+02;
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Sciurognathi;
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ches 0;
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                                             Embryophyta; Trach
a; Poales; Poaceae;
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                                                                 Tracheophyta;
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RESULT OR RESULT
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Q92HH2
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Rickettsiaceae;
NCBI_TaxID=781;
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Q1-DEC-2001
Q1-DEC-2001
Q1-DEC-2001
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                      Eukaryota;
Mammalia; E
                                                                                                       01-NOV-1998 (TremBLrel.
01-NOV-1998 (TremBLrel.
01-JUN-2001 (TremBLrel.
GM3 SYNTHASE (EC 2.4.99.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein; Complete SEQUENCE 296 AA; 33899 MW;
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Samson D., Roux V.,
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Bacteria; Proteobacteria; alp
Rickettsiaceae; Rickettsieae;
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                                                               Mus musculus (Mouse)
                                                                                     SIAT9
                                                                                                                                                                                         088829;
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EMBL; AE008635; AAL03337.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21442074; PubMed=11557893;
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SEQUENCE FROM N.A.
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                      Metazoa;
Eutheria;
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nilarity 75.0%;
Conservative
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                        Chordata;
Rodentia;
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Cossart P., Weisse
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87.5%;
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eae; Rickettsia.
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Last annotation updat
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Pred. No. 1.2e+02;
                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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Weissenbach J., Claverie
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1.5e+02;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (ALPHA-2,3-SIALYLTRANSFERASE (EC 2.
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SEQUENCE FROM N./
STRAIN=C57BL6J;
                                                                                                                                                                                   Mus musculus (Mouse).
Mus musculus (Mouse).
Mus musculus (Mouse).
Mus musculus (Mouse).
Metazoa; Chordata;
Metazoa; Rodentia;
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"Expression cloning of mouse cDNA of CMP-MeuAc: lactosylceramide alpha2, 3sialyltransferase (GM3 synthase), the enzyme that initiat the synthesis of gangliosides).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (SEP-1998) [2]
                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kapitonov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-BALB-C
                                                                                                           Biochem. Biophys. Res. Commun. 253:17
EMBL; Y15003; CAA75236.1; -.
MGD; MGI:1339963; Siato;
InterPro; IPR001675; Glyco_transf_29; 1.
Pfam; PF00777; Glyco_transf_29; 1.
Transferase; Glycosyltransferase.
                                                                                                                                                                                                                                                                             STRAIN=ICR; TISSUE=BRAIN;
MEDLINE=99092398; PubMed=9875239;
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"Combinatorial PCR
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AB013302; BAA76467.1; -.
AF119416; AAF66147.1; -.
MGI:1339963; Siat9.
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                 Conservative
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               Score 31; DB Pred. No. 1.8e 0; Mismatches
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Pred.
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                                                                                               8E3C734CD1899E3C CRC64;
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             1.8e+02;
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01-MAR-2001
01-MAR-2001
01-JUN-2001
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio Sakai K., Okido T., Furuno M., Aono H., Baddarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.
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O1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SIALVLIRRANSEERASE 9 (CMP-NEUAC:LACTOSYLCERAMIDE ALPHA-2,
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Nature 407:508-513(2000).

EMBL; AL445065; CAC11845.1; -.

InterPro; IPR001296; Glycos_transf_1.

Pfam; PF00534; Glycos_transf_1; 1.

Hypothetical protein; Complete proteome.

SEQUENCE 384 AA; 44734 MW; BEC8D05CF0237E40 CRC64;
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                                                                                                                                                                           SEQUENCE PROM N.A.
STRAIR-C57BL/6J; TISSUE-EMBRYO;
STRAIR-C57BL/6J; PubMed=11217851;
MEDLINE=2108560); PubMed=11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Kawai J., Fukuda Aizawa K., Hara A., Fukunishi K., Konno H., Adachi J., Fukuda Arakawa T., Hara A., Fukunishi K., Kiyosawa H., Kondo S., Yamanaka Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito
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Mammalia; Eutheria;
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Archaea; Euryarchaeota; Thermoplasmales; Thermoplasmaceae;
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Rodentia;
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Fukuda S.,
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Q9QWF9;
Q1-MAY-2000 (TrEMBLrel. 13, Createq)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-MAY-2001 (TrEMBLrel. 17, Last annotation update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Q1-JUN-2001 (TrEMBLRel. 17, Last annotation update)
                                01-DEC-2001
01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                             InterPro; IPR001675; Glyco_transf_29.
Pfam; PF00777; Glyco_transf_29; 1.
Transferase; Glycosyltransferase.
SEQUENCE 387 AA; 44562 MW; CBD1ECDF5E390ACB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                            Q91GJ3
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MGD; MGI:1339963;
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                       DNAPOL.
                                                                   Q91GJ3;
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                                                                                                                                                                                                                                                                                                                                                              STRAIN=ICR; TISSUE=BRAIN; MEDLINE=99092398; PubMed=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Functional annotation of a full-length mouse Nature 409:685-690(2001).
EMBL; AK012961; BAB28571.1; -.
MGD; MGI:1339963; Siat9.
InterPro; IPR001675; Glyco_transf_29.
Pfam; PF00777; Glyco_transf_29; 1.
SEQUENCE 387 AA; 44572 MW; 7D358298034CDD5
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                    368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             368
                                                                                                                                                                                         Local
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postvittana
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                                                                            PRELIMINARY;
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nucleopolyhedrovirus
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Pred. No.
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annotation update)
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1.9e+02;
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1.9e+02;
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v; GM3 synthase).";
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Best Local S
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Best Local
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ProDom; PD001202; PI_PIC_Y; 1.
SMART; SM00129; C2; 1.
SMART; SM00149; PLCYC; 1.
SMART; SM00149; PLCYC; 1.
SMART; SM00149; PLCYC; 1.
PROSITE; PS50004; C2_DOMAIN 2; 1.
PROSITE; PS50007; PIPIC_X_DOMAIN; 1
PROSITE; PS50008; PIPIC_X_DOMAIN; 1
PROSITE; PS50008; PIPIC_X_DOMAIN; 1
PROSITE; PS50008; PIPIC_X_DOMAIN; 1
                                                                                                                                                                                                                                                                                                                                   (1)
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=96257751; PubMed=8687401;
Waldo G.L., Paterson A., Boyer J.L.,
Waldo G.L., Cloning, expression and refinitiated ph
                                                                                                                                                                                                                                                                                 Luccnem. J. 316:559-568(1996).
EMBL; U49431; AAC60011.1; -.
HSSP; P10688; 1QAS.
                                                                                                                                                                                                        Pfam; PF00168; C2; 1.
Pfam; PF00388; PI-PLC-X; 1.
Pfam; PF00387; PI-PLC-Y; 1.
                                                                                                                                                                                                                                        InterPro; IPR000008; C2.
InterPro; IPR001192; PI_PLC.
InterPro; IPR000909; PI_PLC_X.
InterPro; IPR001711; PI_PLC_Y.
                                                                                                                                                                                                                                                                                                            erythrocytes.
Biochem. J. 3
                                                                                                                                                                                                                                                                                                                                                                                                              Meleagris gallopavo (Common turkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Archosauria; Aves; Neognathae; Galliformes; Meleagri
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01-NOV-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleopolyhedrovirus genome.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AY042265; AR885622.1; -
SEQUENCE 960 AA; 111520 MW; OCBBABEZEOF5B540 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9103;
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KLFLKLLK
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                                            Similarity 7; Conserv
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                                           Score 31; DB
Pred. No. 5.26
0; Mismatches
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Last annotation updat
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Pred. No. 4.3e
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                                                                                                                                                                                                                                                                                                                                  L., Nicholas R.A., Harden T.K.; d regulatory activity of G alpha phospholipase C-beta from avian
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. 4.3e+02;
0;
                                                      DB 13;
5.2e+02;
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                                                                Length 1211;
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                                                                                                   CRC64;
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096DS1 PRDATE OPERATED OPERATE
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096DS5;
01-DEC-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
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Bartel F., Taylor A.C., Taubert H., Harris L.C.
"Novel mdm2 splice variants identified in pedia
tumors and cell lines.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ d
EMBL; AF385324; AAL13244.1; -.
SEQUENCE 66 AA; 7396 MW; E3B3F3C385D4A8A5 C
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MDM2.
Homo sapiens (Human).
Homo rvota; Metazoa; Chordata; Metazoa; Primates;
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Bartel F., Taylor A.C., Taubert H., Harris L.C.;
"Novel mdm2 splice variants identified in pediatric rhab
tumors and cell lines.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF385322; AAL13242.1;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TremBLrel.
01-DEC-2001 (TremBLrel.
01-DEC-2001 (TremBLrel.
MDM2 VARIANT FB28.
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100.0%; Pr
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Last sequence update)
Last annotation update)
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pediatric rhabdomyosarcoma
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Job time: 296 sec
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Bartel F., Taylor A.C., Taubert H., Harris L.C.;
"Novel mdm2 splice variants identified in pediatric rhab
tumors and cell lines.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF385326; AAL13246.1;
SEQUENCE 95 AA; 10622 MW; 00052F95211E3612 CRC64;
                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                        NCBI_TaxID=9606; [1]
                                                           33 LLLKLLK
                                                                                  2 LLLKLLK 8
                                                                                                          Similarity 7; Conserv
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100.0%;
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Pred. No.
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Copyright (c) 1993
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/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
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US-08-245-500A-5
US-08-390-546-5
US-08-390-517A-5
US-08-390-515A-5
US-08-390-515A-3
US-08-245-500A-3
US-08-390-546-3
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Patent No. 6280989

GENERAL INFORMATION:

APPLICANT: Kapitonov, Dmitri

APPLICANT: Yu, Robert

TITLE OF INVENTION: NOVEL SIALYLTRANSFERASES

FILE REFERNCE: VCUIP-6

CURRENT APPLICATION NUMBER: US/09/334,601

CURRENT FILING DATE: 1999-06-17

NUMBER OF SEQ ID NOS: 94

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 4

LENGTH: 414

TYPE: PRT

ORGANISM: Murinae gen. sp.

US-09-334-601-4
                                                                                                                                                                                                                                                                    RESULT 2
US-07-725-331-9
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Thehes 7; Conserve
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US-09-334-601-4
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                                                                                                                                                                                                                                        Sequence 9, Application US/07725331 Patent No. 5294605
                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler,
ADDRESSEE: & Milnamow
                                                                     STREET: 180 NO CITY: Chicago STATE: IL
                                                                                                                                                                                                                                                                                                                       395 KFLLKLLK 402
                                           COUNTRY: UZIP: 60601
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                                                        USA
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US-09-115-737-138
US-07-725-331-1
US-08-569-188-8
PCT-US91-05047-1
PCT-US91-05047-1
PCT-US94-07019-8
US-07-725-331-4
US-08-569-188-1
US-08-569-188-1
US-08-569-188-11
US-08-569-188-11
US-08-569-188-12
US-08-569-188-13
PCT-US91-05047-4
PCT-US91-07019-1
PCT-US94-077019-10
PCT-US94-077019-11
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Pred. No. 2.1e+02;
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Result No.

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Minimum

Maximum

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Sequence:

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SOFTWARE: PatentIn Release #1.24 CURRENT APPLICATION DATA:

OPERATING SYSTEM: SOFTWARE: Patentl

PC-DOS/MS-DOS

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US-07-725-331-9
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Best Local
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                                                           APPLICATION NUMBER: PCT/US91/05047
FILING DATE: 19910717
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 3126165460 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
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APPLICATION NUMBER: US 07/554,422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 19-JUL-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                           SOFTWARE: PatentIn Rel
                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Amphiphilic Peptide Compositions and TITLE OF INVENTION: Analogues Thereof
                                                                                                                                                                                                                                                                                                               STREET: ____
                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/07/725,331
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 42
ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.24
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                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Dressler, Goldsmith, Sutker, Shore ADDRESSEE: & Milnamow
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Blondelle, Sylvie
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; TOPOLOGY: 1; MOLECULE TYPE: US-08-944-133-13
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Matches 7
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                     TELEFAX: 504 346-8049
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: McLaughlin, Mark
APPLICANT: Becker, Calvin L
TITLE OF INVENTION: Amphipat
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
                                                                                                                                                   NAME: Runnels, John H
REGISTRATION NUMBER: 33451
REFERENCE/DOCKET NUMBER: At:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 504 387-3221
                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 5530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/789,077
FILING DATE: 03-FEB-1997
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                       FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Runnels, John H
                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
COUNTRY: USA
7TP: 70821-2471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: May be a C-terminal amide, and/or may OTHER INFORMATION: be acetylated at N-terminus, Xaa is OTHER INFORMATION: Met or methionine sulfoxide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC
OPERATING SYSTEM:
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TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/0:
FILING DATE: 06-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: P. O. Box CITY: Baton Rouge
                                                 LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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7; Conserv
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P. O. Box 2471
                                                                                                                                       504 346-8049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                         Atty File No. 5789542 9301
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Pred. No. 19;
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ADDRESSEE:

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                                                                                                                                 US-07-903-103-4
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US-08-248-839C-47
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Best Local S
Matches 7
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                                                                                                   Sequence 4, Application US/07903103 Patent No. 5411860
                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                              Query Match
       GENERAL INFORMATION:
APPLICANT: VOGELSTEIN, BERT
APPLICANT: KINZLER, KENNETH
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
TITLE OF INVENTION: HUMAN TUMORS
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/
FILING DATE: 25-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta A.
REGISTRATION NUMBER: 35,12
REFERENCE/DOCKET NUMBER: 35,12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
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APPLICANT: Devine, Kevin
APPLICANT: O'Kane, Charles
TITLE OF INVENTION: A Gene Expression System
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 86 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                          49 KIVLKLLK 56
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                                                                                                                                                                                                                                                  Local Similarity es 6; Conserv
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7; Conser
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Pred. No.
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Pred. No.
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Best Local Similarity
Watches 7; Conserva
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/044,619A
FILING DATE: 07-APR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/903,103
FILING DATE: 23-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                        APPLICANT: THE JOHNS
APPLICANT: 720 RUTLA
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                           COUNTRY: USA
ZIP: 20001-4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
ADDRESSEE: 1001 G ST., N.W.
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REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/867.840
FILING DATE: 07-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                     CITY: WASHINGTON
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CITY: WASHINGTON
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                                                                                                                                                                                                                                                                                                                                                                          THE JOHNS HOPKINS UNIVERSITY
720 RUTLAND AVENUE, BALTIMORE, MARYLAND 21205 USA
VENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                           HUMAN TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85.7%; Score 30; 100.0%; Pred. No.
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Best Local Similarity 100.
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08283911 Patent No. 5519118
                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 23-UN-1992
APPLICATION NUMBER: US 07/
FILING DATE: 07-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: VOGELSTEIN, BERT
APPLICANT: KINZLER, KENNETH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 202-508-9299
TELEX: 197430 BBMB UT
INFORMATION FOR SEQ ID NO:
                                                               NFORMATION FOR SEQ ID NO:
               SEQUENCE CHARACTERISTICS:
LENGTH: 489 amino acids
TYPE: amino acid
                                                                                                           TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: protein
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
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                                                                          TELEFAX: 202-508-9299
TELEX: 197430 BBMB UT
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/283,911 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: WASHINGTON STATE: D.C.
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            amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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%; Pred. No. 3.6
0; Mismatches
                                                                                                                                            01107.40148
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RESULT 10 US-08-390-546-5

Sequence 5, Applic Patent No. 5606044

Application US/08390546

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GENERAL INFORMATION: APPLICANT: BURREL!

BURRELL, MARILEE HILL, DAVID E.

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                                      Query Match
Best Local Similarity
Thes 7; Conserv
                                                                                                                      ; MOLECULE TYPE: US-08-245-500A-5
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Best Local Similarity
"hes 7; Conservations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
                                                                                                                                                                                      TELEX: 197430 BBMB UT INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 07-APR-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: LULL
CTTY: WASHINGTON
33 LLLKLLK 39
                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                              TELEFAX:
                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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                         2 LLLKLLK 8
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                                                                                                                                                            amino acids
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                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KINZLER, KENNETH W.
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                                                                                                                                                                                                                                                                                                                                                                                           IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                  linear
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                                                                                                                                   protein
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DAVID E.
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                                                85.7%; Score 30;
100.0%; Pred. No.
Live 0; Mismatc
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100.0%; Pred. No.
tive 0; Mismatc
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                                                                                                                                                                                                                                                                                                                                                   US/08/245,500A
                                                                                                                                                                                                                                                                                   32,141
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                                                    Mismatches
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3.6e+02;
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                                                              3.6e+02;
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Score 30; Pred. No. Mismatches

DB 1; 3.6e+02;

Length 489;

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Gaps

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01107.48992

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Query Match
Best Logal Similarity
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US-08-390+546-5
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                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 202-508-9299
TELEX: 197430 BBMB UT
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
STREET: 1001 G STREET, NOW.
                                                                           MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
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             SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                              APPLICANT: VOGELSTEIN, BERT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                             CITY: WASHINGTON
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                                                                                                                                            STATE: D.C
                                                                                                                             COUNTRY: USA
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1001 G STREET, N.W.
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100.0%; Pr
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US/08/390,479A
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Pred. No.
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3.6e+02;
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Best Local Similarity
7; Conserve
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US-08-557-393-5
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                                                                         TELEFAX: 202-508-9299
TELEX: 197430 BBMB UT
INFORMATION FOR SEQ ID NO:
                                                                                                                                       APPLICATION NUMBER: US 08/245
FILING DATE: 18-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 0110
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 489 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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                                           SEQUENCE CHARACTERISTICS:
LENGTH: 489 amino acid
                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: KINZLER, KENNETH W. APPLICANT: VOGELSTEIN, BERT
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33 LLLKLLK 39
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TELEX: 197430 BBMB UT
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                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 13-NOV
                                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: WASHINGTON STATE: D.C.
                                                                                                             TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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               TOPOLOGY:
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                                             489 amino acids
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202-508-9299
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                                                                                                                                                                                                                                                                                                                                                         IBM PC compatible SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
                                                                                                                                                                                                                                                                                           13-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DAVID E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HUMAN TUMORS
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100.0%;
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Version #1.25

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RESULT 14
US-08-390-517A-5
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Best Local Similarity
"~+~hes 7; Conserv?
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US-08-390-516C-5
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                          Sequence 5, Application US/08390517A Patent No. 5736338 GENERAL INFORMATION:
                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/08390516C Patent No. 5708136 GENERAL INFORMATION:
                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                   TELEX: 197430 BBMB UT
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                     NAME: KAGAN, SARAH A.
REGISTION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01:
TELECOMMUNICATION INFORMATION:
                APPLICANT:
                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 489 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: AMPLIFICATION HUMAN TUMORS
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                                                                                                                      33 LLLKLLK
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 BURRELL, MARILEE HILL, DAVID E.
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KINZLER, KENNETH W.
VOGELSTEIN, BERT
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                                                                                                                                                                                                                                                                    linear
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100.0%; Pr
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Pred. No.
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Pred. No.
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                                                                                                                                                                                    DB 1; L, 3.6e+02;
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3.6e+02;
                                                                                                                                                                                               Length 489;
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                                                                                                                                                                        Indels
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RESULT 15
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 489 amin-
TYDD:
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APPLICANT: VOGELSTEI
TITLE OF INVENTION:
TITLE OF INVENTION:
             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                APPLICANT: BURRELL, MARILEE
APPLICANT: HILL, DAVID E.
APPLICANT: KINZLER, KENNETH W.
APPLICANT: VOGELSTEIN, BERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,517A
FILING DATE: 07-APR-1993
CLASSIFICATION: 435
CLASSIFICATION: 435
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-5100
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NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                  CITY: WASHINGTON STATE: D.C.
                                                                                                                                 COUNTRY:
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amino acid
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100.0%; Pred. No. 3.6e+02;
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US/08/390,515A
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FILING DATE: 07-APR-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.42798
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELLEPAX: 202-508-9299
TELEEX: 197430 BBMB UT
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 489 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-390-515A-5

Ouery Match
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
Oy 2 LLLKLLK 8
US-08-391-11111
Db 33 LLLKLLK 8
Search completed: June 17, 2002, 12:42:05

Search completed: June 17, 2002, 12:42:05
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Result
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Maximum Match 100%
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Copyright (c) 1993 - 2000 Compugen Ltd.
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AAB17122	AAR67795	AAP91335	AAW77384	ABB64083	AAB52057	AAY49957	AAW65895	AAY29393	ААВ60066	AAU03187	AAB17422	AAB17421	AAB17420	AAB17417	AAB17414	AAW82887	AAW82886	AAW82885	AAW82857	AAW82851	AAW82848	AAW35171	AAW35170	AAW35169	AAW35153	AAW35150	AAW77378	AAB17485	AAB17483	AAB17416	AAB17413	285	AAW82850	
Calmodulin antagon	Antimicrobial olig		Lytic peptide with	Drosophila melanog	ct		Amphipathic peptid	Sperm whale myoglo		rane active											ᠴ				Leu/Lys diastereom	s diaste	Lytic peptide with	Antipathogenic pep					Antipathogenic pep	

ALIGNMENTS

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AAW82854 standard; peptide;

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AAW82854;

19-MAY-1999

(first entry)

Antipathogenic peptide.

WPI; Oren Non-haemolytic; cytolytic; selective cytolytic activity; pathogen; cancer; infection; disinfectant; contact lens wetting solution; preservative; pesticide; fungicide; bactericide. W09837090-A1 Synthetic. 20-FEB-1997; 19-FEB-1998; 27-AUG-1998 (YEDA) YEDA RES & DEV CO LTD. 1998-594464/50 Shai Y; 97WO-IL00066. 98WO-IL00081

New non-haemolytic cytolytic agent useful in treating cancer infections - is a peptide comprising a moiety which disrupts continuity of an alpha-helical structure

or

Claim 14;

Page

106;

126pp; English

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                                                                                                         New non-haemolytic cytolytic agent useful in treating cancer or infections - is a peptide comprising a moiety which disrupts the continuity of an alpha-helical structure
                                                                         Claim 17; Page 106; 126pp; English
                                                                                                                                                                                                          WPI; 1998-594464/50.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  27-AUG-1998
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tion; disinfectant; contact lens wetting solution;
pesticide; fungicide; bactericide.
                                                                                                                                                                                                                                                                                                                                         97WO-IL00066.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptide;
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specification describes a non-haemolytic, peptide, a complex of bundled peptides, a

peptide is used to produce the agents of the invention. The on describes a non-haemolytic, cytolytic agent, which is a complex of bundled peptides, a mixture of peptides or a random

The present peptide is used to produce the agents of the invention. The specification describes a non-haemolytic, cytolytic agent, which is a peptide, a complex of bundled peptides, a mixture of peptides or a random peptide copolymer. The agent has a selective cytolytic activity on pathogenic cells. The agent is selected from a cyclic derivative of a peptide which has a net positive charge greater than 1, comprises I-amino acid residues and/or D-amino acid residues and comprises an alpha-helix breaker moiety, or a peptide (or cyclic derivative of this) which

Page 106; 126pp; English

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Best Local
                                                                                                                                      New non-haemolytic cytolytic agent useful in treating cancer or infections - is a peptide comprising a moiety which disrupts the continuity of an alpha-helical structure
                                                                                                                                                                                                    WPI; 1998-594464/50.
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                                                                                                                                                                                                                                                                                                             19-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Non-haemolytic; cyt cancer; infection;
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                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                          preservative;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW82855 standard; peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a corresponding amino acid sequence comprising only L-amino acid residues is not found in nature. The cytolytic agents may be used for treatment of cancer or for treatment of several diseases caused by pathogens, including bacterial, fungal, viral, mycoplasma and protozoan infections. They may be used in both human and veterinary medicine. They may also be solutions for wetting contact lenses, as preservatives, e.g., in the cosmetic and food industries, as pesticides (e.g. fungicides or bactericides) or for preservation of agricultural products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide copolymer. The agent has a selective cytolytic activity on pathogenic cells. The agent is selected from a cyclic derivative of a peptide which has a net positive charge greater than 1, comprises L-amin acid residues and/or D-amino acid residues and comprises an alpha-helix breaker moiety, or a peptide (or cyclic derivative of this) which (comprises L-amino acid residues and D-amino acid residues, has a net positive charge greater than 1 and has an amino acid sequence such that
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                                                                                                                                                                                                                                                                                                                                                                                                                        pesticide;
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                                                                                                                                                                                                                                                                                                                                                                                                               cytolytic; selective cytolytic activity; pathogen; on; disinfectant; contact lens wetting solution; esticide; fungicide; bactericide.
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specification describes a non-haemolytic, cytolytic agent, which is a peptide, a complex of bundled peptides, a mixture of peptides or a random peptide copolymer. The agent has a selective cytolytic activity on pathogenic cells. The agent is selected from a cyclic derivative of a peptide which has a net positive charge greater than 1, comprises L-amino acid residues and/or D-amino acid residues and comprises an alpha-helix (comprises L-amino acid residues and D-amino acid residues, has a net positive charge greater than 1 and has an amino acid sequence such that a corresponding amino acid sequence comprising only L-amino acid residues is not found in nature. The cytolytic agents may be used for treatment of several diseases caused by pathogens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New non-haemolytic cytolytic agent useful in treating cancer infections - is a peptide comprising a moiety which disrupts continuity of an alpha-helical structure
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17; Page 107; 126pp; English.
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infection; disinfectant; contact lens wetting solution;
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92.9%;
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Pred. No. 0.0053;
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This sequence represents a diastereomer peptide of the invention. This sequence is used in a "bundle sequence", which is created by binding copies of this sequence to peptide 23 (see AAW35149). The peptides of the invention have: (a) cytolytic activity on pathogenic cells (pathogand malignant cells not naturally present in the body); but (b) no haemolytic activity, or such activity only at a concentration significantly higher than that at which they lyse pathogens. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
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                                                                                                                                                                                                                                                               Peptide(s) having selective cytolytic activity - and malignant cells, but no haemolytic activity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-FEB-1996;
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                                                                                                                                                                                                                                           and
                                                                                                                                                                                            Page 49; 80pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pesticide; cell wall lysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide
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                                                                                                                                                                                                                                           cancer
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92.9%;
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                                                                                                                                                                                            English
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Pred. No. 0.025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19;
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                                                                                                                                                                                                                                                                  against pathogens
used for treating
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may also be
                                                                        (pathogens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local 9
The present invention describes composition of matter (I) comprising of comain, pharmacologically active peptides, and linkers. Where (I) (X1)a-F1-(X2)b, where: F1 = an Fc domain, X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, (L4)f-P4 (L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 (L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 (L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 (L2)d-P2-(L3)e-P3-(L4)f-P4 (L2)d-P2-(L3)e-P3-(L4)f-P4 (L2)d-P2-(L3)e-P3-(L4)f-P4 (L2)d-P3-(L4)f-P4 (L2)d-P3-(L4)f-P4 (L2)d-P3-(L4)f-P4 (L3)d-P3-(L4)f-P4 (L3)d-P3-(L4)f-P4 (L3)d-P3-(L4)f-P4 (L4)d-P3-(L4)d-P3-(L4)f-P4 (L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)
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                                                                                                                                                                                                         Claim 39; Page 401; 608pp; English.
                                                                                                                                                                                                                                                           autoimmune diseases
                                                                                                                                                                                                                                                                        Novel composition of matter comprising an pharmacologically active peptides, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AMGE-) AMGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         asthma; thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified peptide; therapeutic agent; fusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB17482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB17482 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MMP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 KLLLKLLKLLKC 14
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                                                                                                                                                                                                                                                                                                                                                              2000-350702/30.
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99US-0428082.
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                                                                                                                                                                                                                                                                                                                                                                                                                Cheetham
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87.1%;
100.0%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                             Boone
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0.013;
                                                                                                                                                                                                                                                                             fc domain and
for treating or
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This sequence sequence is us

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peptide
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created the

invention. The

Example 7; Page 50; 80pp; English.

and cancer

Peptide(s) having selective cytolytic activity - against pathogens and malignant cells, but no haemolytic activity, used for treating

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RESULT
AAW35232
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Best Local :
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                                                                                                        WPI; 1997-435088/40
                                                                                                                                 Oren
                                                                                                                                                       (YEDA ) YEDA RES & DEV CO LTD
                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                      Diastereomer peptide; infection; therapy; excitatory neurotoxin; Honey bee venom; pardaxin; cytolytic activity; cancer; non-haemolytic; preservative; agricultural produce; bacterial cell lysis; agricultural pesticide; cell wall lysis.
                                                                                                                                                                                22-FEB-1996;
                                                                                                                                                                                                       20-FEB-1997;
                                                                                                                                                                                                                               28-AUG-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
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10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide; 13 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [D]-L3,4,8,10-K5L7C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
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                                                                                                                                                                                                                                                                            "D-form residue"
                                                                                                                                                                                                                                                                                                    "D-form residue"
                                                                                                                                                                                                                                                                                                                           "D-form
                                                                                                                                                                                                                                                                                                                                                  "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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Pred. No.
                                                                                                                                                                                                                                                                                                                          residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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0.013;
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RESULT
AAB17484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches · 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified peptide; therapeutic agent; fusion; Fc domain; cance autoimmune disease; cytostatic; antiasthmatic; thrombolytic; immunosuppressive; EPO; TPO; CTLA4; mimetic; II-1; TNF; antac MMP; 'inhibitor; erythropoietin; thrombopoietin; therleukin I cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor
The present invention describes composition of matter (I) FC domain, pharmacologically active peptides, and linkers.
                                                                                                                                       Claim 39;
                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-350702/30.
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                                                                                                                                                                                                                                                                     Novel composition of matter comprising an pharmacologically active peptides, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AMGE-) AMGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-OCT-1998;
22-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antipathogenic peptide sequence SEQ ID NO:588.
                                                                                                                                                                                                                                                            pharmacologically active
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99US-0428082
                                                                                                                                       401;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13
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                                                                                                                                  608pp; English
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92.3%;
                                                                                                                                                                                                                                                                 peptides,
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Boone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thrombopoietin; interleukin 1;
igen 4; tumour necrosis factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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0.094;
                                                                                                                                                                                                                                                            Fc domain and
for treating 
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comprising . Where (I)

is

Peptide(s) having selective cytolytic activity - against pathogens

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RESULT
AAW35149
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(X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each clindependently selected from -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4.

(L1)c-P1-(L2)d-P2-(L3)e-P3-(D3)e-P3-(D3)e-P3-(L4)f-P4.

(C) where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently composition can be used for producing pharmaceutical compositions. The composition can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombols, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein Abinding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                   Leu/Lys diastereomer peptide; infection; therapy; excitatory neurotoxin; Honey bee venom; pardaxin; cytoclytic activity; cancer; non-haemolytic; preservative; agricultural produce; bacterial cell lysis agricultural pesticide; cell wall lysis.
                           WPI; 1997-435088/40
                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                  Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
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                                                                               (YEDA ) YEDA RES & DEV CO LTD
                                                                                                            22-FEB-1996;
                                                                                                                                      20-FEB-1997;
                                                                                                                                                                28-AUG-1997
                                                                                                                                                                                            WO9731019-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leu/Lys diastereomer peptide [D]-L3,4,8,10-K4L8.
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92.3%;
                                                                                                                                                                                                                        "C-terminal amide"
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                                                                                                                                                                                                                                                                                                                                    "D-form residue"
                                                                                                                                                                                                                                                  "D-form residue"
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                                                                                                                                                                                                                                                                                                                                                                                                                                     cell lysis;
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Best Local S
Matches 12
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WO9731019-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            increased resistance to proteolytic degradation. Non-haemolytic, cytotoxic random copolymers of pardaxin, each has a specific spectru activity, allowing selection of agents for particular applications. these random copolymers induce total lysis of bacterial cell walls, resistance to them is unlikely to develop.
                                                                                                     Misc-difference
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                                                                                                                                                                                  Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 non-haemolytic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /s diastereomer peptide; infection; therapy; excitatory neurotoxin;
bee venom; pardaxin; cytolytic activity; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21; Page 39;
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12; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ic; preservative; agricultural produce;
pesticide; cell wall lysis.
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                                                                                            W09837090-A1
                                                                                                                         Synthetic
                                                                                                                                                Non-haemolytic; cytolytic; selective cytolytic activity; pathogen; cancer; infection; disinfectant; contact lens wetting solution; preservative; pesticide; fungicide; bactericide.
                                                                                                                                                                                                                                                                                                AAW82847 standard; peptide;
           20-FEB-1997;
                                        19-FEB-1998;
                                                                    27-AUG-1998
                                                                                                                                                                                                              Antipathogenic
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ilarity 100.0%.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          used as disinfectants for destruction of microorganisms, i.e. solutions for wetting contact lenses, as preservatives, e.g., cosmetic and food industries, as pesticides (e.g. fungicides c bactericides) or for preservation of agricultural products.
WPI; 1998-594464/50
                               Oren Z,
                                                             (YEDA ) YEDA RES & DEV CO LTD
                                                                                              20-FEB-1997;
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                                                                                                                                                                                                                                                       preservative;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             specification describes a non-haemolytic, cytolytic agent, which is a peptide, a complex of bundled peptides, a mixture of peptides or a random peptide copolymer. The agent has a selective cytolytic activity on pathogenic cells. The agent is selected from a cyclic derivative of a peptide which has a net positive charge greater than 1, comprises L-amino peptide which has a net positive charge greater than 1, comprises L-amino
           New non-haemolytic cytolytic agent useful in treating cancer or infections - is a peptide comprising a moiety which disrupts th continuity of an alpha-helical structure
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Claim 14; Page 106; 126pp; English

peptide is used to produce the agents of the invention.

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             autoimmune diseases
                 Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating
                                                                                                                                                                                                                                                                                                                                                                                             Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; CTLA4; mimetic; TL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                               WPI; 2000-350702/30.
                                                                                                                                                                                          23-OCT-1998;
22-OCT-1999;
                                                                                                                                                       (AMGE-) AMGEN INC
                                                                                                                                                                                                                                               25-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antipathogenic peptide sequence SEQ ID NO:517.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each (X1)a-F1-(X2)d-P2-(L3)a-P3, or -(L1)c-P1-(L2)d-P2-(L4)d-P2-(L3)a-P3, or -(L1)c-P1-(L2)d-P2-(L4)f-P4 (X1)a-P1-(L2)d-P2-(L4)f-P4 (X2)a-P3 (Y2)a-P3 (Y3)a-P3 (Y4)f-P4 (Y3)a-P3-(Y4)f-P4 (Y3)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3-(Y4)a-P3
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Best Local
                                          autoimmune diseases
                                                   Novel composition of matter comprising an Fc domain pharmacologically active peptides, useful for treats
                                                                                                                                                                                                                                                               23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNP; antagonist; MMP; inhbitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                WPI; 2000-350702/30
                                                                                                                                                                                                                  (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                             04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                       WO200024782-A2
                                                                                                                                                                                                                                                                                                                              25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antipathogenic peptide sequence SEQ ID NO:520.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB17416 standard; Peptide; 12 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes composition of matter (I) comprising FC domain, pharmacologically active peptides, and linkers. Where (I)
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99US-0428082.
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100.0%; Pr
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0.23;
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Claim 39; Page 379; 608pp; English

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The present invention describes composition of matter (I) comprising an CC (X1)a-FI-(X2)b, where: FI = an FC domain; X1 and X2 = are each CC (X1)a-FI-(X2)b, where: FI = an FC domain; X1 and X2 = are each CC independently selected from -(L1)c-P1 -(L1)c-P1-(L2)d-P2 (L3)e-P3-(L4)f-P4 (CC vhere P1 - P2 P3 and P4 = are each independently sequences of CC pharmacologically active peptides; L1, L2, L3, and L4 = are each independently condensed that at least 1 of a and b is 1. The composition can CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can CC be useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer CC half-life or incorporate functions such as Fc receptor binding, complement fixation, and possibly placental transfer. AAA69443 CC sequences used in the exemplification of the present invention acid con aAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid con sequences used in the exemplification of the present invention.
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X202020202020202020X

Sequence 12 AA;

Query Match . 74.3%; Score 52; DB 21; Length 12; Best Local Similarity 100.0%; Pred. No. 0.23; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Search completed: June 17, 2002, 12:41:23 Job time: 298 sec

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Perfect score:
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       June 17, 2002, 12:43:01; Search time 46.42 Seconds (without alignments) 28.980 Million cell up
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probable ABC
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50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	51.4	51.4	51.4	51.4	51.4
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T19116	T18924	A70102	C81386	A49762	C84647	E75204	H84493	B72717	I50498	G85837	T01490	T31330	T17308	AH0031	T20204
hypothetical prote	hypothetical prote	conserved hypothet	probable integral	somatolactin precu	probable synaptobr	hypothetical prote	probable replicati	hypothetical prote	urotensin II-alpha	hypothetical prote	hypothetical prote	head-activator bin	hypothetical prote	proton glutamate s	hypothetical prote

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A; Molecule type: DNA
A; Residues: 1-169 < ARN-A
A; Residues: 1-169 < ARN-A
A; Residues: 1-169 < ARN-A
A; Cross-references: GB: AE001613; GB: AE001363; NID: g4376550; PIDN: AAD18426.1; PID: g437
A; Experimental source: strain CWLO29
A; C:; Dodson, R:; Gwinn, M:; Nelson, W:; DeBoy, R.; Kolonay, J:; McClarty, G:; Salzbe
Nucleic Acids Res. 28, 1397-1406, 2000
A; Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39
A; Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39
                                                                                                                                                                                                                                                                                                                                                              R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis. A;Reference number: A72000; MUID:99206606
A;Accession: G72096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein CP0481 [Imported] - Chlamydophila pneumoniae (strains CWL029 c;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000 C;Accession: G72096; C81573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein Z1386 [imported] - Escherichia coli (strain O157:H7, substrain C;Species: Escherichia coli C;Species: Escherichia coli C;Cate: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C;Cate: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C;Accession: B85632 C;Accession: B85632 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mailler, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apod Mature 409, 529-533, 2001
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A;Reference number: A81500; MUID:20150255
A;Accession: C81573
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A;Gene: Z1386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-38 <STO>
                                                                                                                                                                                                                                                                                                                              A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
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6; Conservative
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Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349
A;Status: nralimits.
                                                               A:Map position: .12R
C:Keywords: transmembrane protei
F:263-279/Domain: transmembrane
                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-314 <PAU>
A; Cross-references: EMBL:U17243;
                                                                                                                                                                                                                C;Species: Saccharomyces cerevisiae
C;Date: 13-Jan-1995 #sequence_revision 20-Feb-1995 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: CPj0277
C;Superfamily: Chlamydia pneumoniae hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein CPj0277 [imported] - Chlamydophila pneumoniae (strain J138) C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-169 <REA>
A;Cross-references: GB:AE002209; GB:AE002161; NID:g7189393; PIDN:AAF38311.1; PID:g7189393;
A;Experimental source: strain AR39, HL cells
                                                                                                              A; Gene: MIPS:YLR283w
                                                                                                                              A;Cross-references:
C;Genetics:
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A; Accession: S50368
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A;Experimental source: strain J138
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A; Residues: 1-169 <STO>
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                                                                                                                                                                                                                                                                                                                 N; Alternate names: hypothetical protein L8003.9
                                                                                                                                                                                                                                                                                                                              probable membrane protein YLR283w - yeast (Saccharomyces cerevisiae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary
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Best Local
      Query Match
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      Similarity
                                                                                                                                                                                                                                                                       S50368
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   57.1%;
58.3%;
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50.0%;
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50.0%;
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Pred.
6; Mis
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Pred. No.
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Pred.
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No.
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 DB
38;
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23;
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23;
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                                                                                                                                                                                                                        cosmid
                                                                                                                                           PID:g596039; GSPDB:GN00012; MIPS:YLR283w
                2;
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                                                                <MMT>
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                Length 314;
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                                RESULT
G85043
hypothetical C; Species: A:
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C; Accession: G95536
C; Accession: G95536
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, C Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, I C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID: 21016719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Hirudo medicinalis (medicinal leecn)
C;Decies: Hirudo medicinalis (medicinal leecn)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-May-2000
C;Accession: T18531
R;Huang, Y; Jellies, J; Johansen, K.M.; Johansen, J.
J. Cell Biol. 138, 143-157, 1997
A;Title: Differential qlycosylation of Tractin and LeechCAM, two novel Ig-s
A;Reference number: Z18951; MUID:97362067
A;Accession: T18531
A;Accession: T18531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein F2J10.9 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_chang
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T18531
                                                                                                                                                                                A; Map position:
                                                                                                                                                                                                                           C; Genetics:
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A; Residues: 1-2513 <STO>
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A; Residues: 1-1880 <HUA>
A; Cross-references: EMBL
                                                                                                                                                                                                     A; Gene: F2J10.9
                                                                                                                                                                                                                                              A;Cross-references:
                                                                                                                                                                                                                                                                                                          A;Status:
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Best Local
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797 LLLGLLLKLLK 807
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                                        3 LLLKLLLKLLK 13
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Hirudo medicinalis (medicinal leech)
                                                                                                                                                                                                                                                                                                          preliminary
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                                                                                                                                                                                                                                              GB:AE005173;
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                                                                                                    57.1%;
90.9%;
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64.3%;
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                                                                              0;
                                                                                                 Score 40;
Pred. No.
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Pred. No.
                                                                                Mismatches
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1.7e+02;
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                                                                                                                     Length 2513;
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R.; Marzia
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al protein AT4g03450 Arabidopsis thaliana

[imported] .

Arabidopsis thaliana

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C;Genetics:
A;Gene: AT4g03450
A;Map position: 4
                                                                           Sur protein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 28-Sep-1990 #sequence_revision 28-Sep-1990 #text_change 21-Jul-2000
C;Date: 35-S60
R;Dorai, T.; Wang, L.H.
Mol. Cell. Biol. 10, 4068-4079, 1990
A;Title: An Biol and the manufacture non-tyrosine protein kinase product of the c-src ger A;Reference number: A35650; MUID:90318371
A;Accession: A35650
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A35650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Experimental source: L1210 leukemia cells LL1 subline A;Note: sequence inconsistent with the nucleotide translation A;Note: sequence extracted from NCB1 backbone (NCBIN:1117028, 1C;Superfamily: AIDS-related virus gag polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    intracisternal A particle GAG protein - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 12-Apr-1995
C;Accession: B44314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Title: Sequence and analysis of chromos
A; Reference number: A85001; MUID:20083488
A; Accession: G85043
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R; anonymous, The Eur
Nature 402, 769-777,
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A;Accession: B44314
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Brigle, K.E.; Westin, E.H.; Houghton, M.T.; Goldman, I.D.
J. Biol. Chem. 267, 22351-22355, 1992
A;Title: Insertion of an intracisternal A particle within the 5'-regulatory region of a ith increased protein expression.
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A; Residues: 1-641 <STO>
A; Cross-references: GB:
                    A; Molecule type: mRNA
A; Residues: 1-219 < DOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA;
A; Residues: 1-30 <BRI>
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    A; Cross-references:
                                                        A; Status: preliminary; not compared with conceptual translation
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Best Local
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sion: G85043
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9; Conser
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GB:M57290; NID:g212703; PIDN:AAA49076.1; PID:g212704
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75.0%;
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70.0%;
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Pred. No. 1e+(
2; Mismatches
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1e+02;
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Query

Match

54.3%;

Score

38;

DВ

2

Length 219;

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hypothetical protein F08B12.3a - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text C;Accession: T20577
                                                           RESULT
T20577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein F08B12.3b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable LRR receptor-like protein kinase [imported] - Arabidopsis thaliana (;Specias: Arabidopsis thaliana (mouse-ear cress) C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001 C;Accession: A85043
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A85043
                                                                                                                         밁
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A; Introns: 38/2; 64/1; 112/2; 148/3; 173/3; 201/3; 348/3;
                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data A; Reference number: Z19295 A; Accession: T20578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Nature 402, 769-777, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B
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                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary;
                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Dobson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T20578
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7; Conserv
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9; Conserv
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be: clone F081
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                                                                                                                                                                                                                                                                                                                                    PIDN:CAA92116.1; GSPDB:GN00028;
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Pred. No. 1.7e
0; Mismatches
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Pred. No.
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2.3e+02;
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1.7e+02;
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                  18-Feb-2000
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A;Cross-references: EMBL:AL031825; PIDN:CAA21231.1; GSPDB:GN00068; SPDB:SPCC757.06 A;Experimental source: strain 972h-; cosmid c757 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-116 <LYN>
                                                                                          A; Status: preliminary; translated
                                                                                                                                      R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Bothe, G.; Pohl, submitted to the EMBL Data Library, October 1998
A;Reference number: Z22003
                                                                                                                                                                                                 hypothetical protein SPCC757.06 - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 C;Accession: T41597
                                                                                                                                                                                                                                                                                   RESULT
T41597
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Best Local Similarity
"hes 7; Conservations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AL592022; PIDN:CAC97648.1; PID:g16414943; GSPDB:GN00178
A;Experimental source: strain Clip11262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A; Authors: Kreft, J; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mc
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AH1734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: lin2421
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A; Residues: 1-83 <GLA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
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A;Introns: 38/2; 64/1; 112/2; 148/3; 173/3; 201/3; 348/3; 392/2; 452/1; 488/2; 538/2; 80
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A;Accession: T20577
A;Status: preliminary; translated from GB/EMBL/DDBJ
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50 MLPLLAKILKC 60
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Pred. No.
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Fsihi, H.
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Search completed: June 17, 2002, Job time: 257 sec

12:43:02

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40

RFLLKLLRKLIK

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uncharacterized protein, Yje/RRF2 family [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 C;Accession: A96914
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, F.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacter A;Reference number: A96900; MUID:21359325; PMID:21359325
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                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
A96914
                                                                                                                  A; Gene:
                                                                                                                                              A;Cross-references: GB:AE001437; PIDN:AAK78100.1; A;Experimental source: Clostridium acetobutylicum
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A; Residues: 1-137 <KUR>
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A;Map position: 3
A;Introns: 10/3; 48/3
                                 Query Match
Best Local S
Matches 8
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Best Local Similarity 40.4
Conservative
                                                                                                                                    Genetics:
                                                 Local Similarity
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2 KLLLKLLKLLK 13
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                                                 52.9%;
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                                             Score 37; DB
Pred. No. 58;
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Pred. No.
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                                                             2;
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                                                                                                                                              PID:g15022941; GSPDB:GN00168
ATCC824
                               2,
                                                             Length 137;
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                             Indels
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Copyright (c) 1993 - 2000 Compugen Ltd
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                                 PRRA_RAT
RPSE_CLOAB
SHBG_RAT
XTMB_BACSU
CDS1_SCHPO
                                                                                                                                                                                                              SOML_HIPHI
SOML_SOLSE
SOML_PAROLI
PRRI_BOVIN
Y147_MYCGE
CCAH HUMAN
UR2A_CYPCA
SOML_GADMO
MTGA_KLEPN
MTGA_KLEPN
YEAST
YDK9_SCHPO
OTOF_HUMAN
RIFI_YEAST
UR2G_CYPCA
IGF_MYXGL
IGF_MYXGL
IGF_MYXGL
IGF_MYXGL
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SOM1_SPAAU
SOM2_SPAAU
SOML_SCIOC
SOML_SIGGU
SOML_CARAU
Y035_TREPA
LP61_EIMTE
COPG_YEAST
EAG_BACSU
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P79894 sparus aura
O9ygk7 sciaenops o
O9pwg4 siganus gut
P79697 carassius a
O83078 treponema p
P15714 eimeria ten
   P20362
P47393
P054180
P05180
P095180
P21919
P48465
P48527
P59539
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2 acipenser t
9 gadus morhu
5 klebsiella
7 saccharomyc
rattus norv
bacillus su
schizosacch
gallus gall
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cyprinus ca
myxine glut
mus musculu
rattus norv
clostridium
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paralichthy
bos taurus
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homo sapie
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SOML_TENU
ID SOML_TENU
ID SOML_TENU
AC Q919H4
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AC Q919H4
DT 01-MAR
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00266; SOMATOTROPIN_1; 1
PROSITE; PS00338; SOMATOTROPIN_2; 1
HOTMONE; Glycoprotein; Signal
SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning and sequencing of Tetraodon miurus somatolactin."; submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: PITUITARY GLAND.
-!- SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tetraodon miurus (Congo puffer).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
NCBI_TaxID-94908;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001400; SOMATOTROPIN. Pfam; PF00103; hormone; 1. PRINTS; PR00836; SOMATOTROPIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence up
01-MAR-2002 (Rel. 41, Last annotation
Somatolactin precursor (SL).
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Rand-Weaver M., May D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                     IEILLKLLKC
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SOMATOLACTIN.
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OF THE PROPERTY OF THE PR
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ACH2_DROME
PURL_BACSU
TRKB_MOUSE
TRKB_RAT
                                                                                                                                                                            Score 40; DB Pred. No. 12; 3; Mismatches
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YO08_BPHP1
PD11_MOUSE
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DPOL_NPVAC
DPOL_NPVBM
CC25_CANAL
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P17644
P12042
P152049
P15209
Q63604
P06738
P18131
P41712
P43069
Q53017
P51709
P56983
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Result

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Query Match

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Database

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Total number of

Searched:

105224 seqs, Gapop

Scoring table: Sequence:

BLOSUM62

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Maximum

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seq

length: length:

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Post-processing: Minimum Match

Maximum

Title: Perfect score:

US-09-367-714A-92

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RESULT
SOM2_SP
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ID DT 0
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Best Local Similarity 70.0
Matches 7; Conservative
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CHAIN
DISULFID
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CARBOHYD
SEQUENCE
"SOM2_SPAAU STANDARD; PRT; 231 AA.
p79904;
p79904;
101-MOV-1997 (Rel. 35, Created)
101-MOV-1997 (Rel. 35, Last sequence update)
101-MAR-2002 (Rel. 41, Last amoutation update)
Sometolactin 2 precursors (SL)
Sparus aurata (Glithead see bream).
Eukaryota: Metacos; Chordata; Craniata; Vertebrata; Euteleostom1;
Actinopterfgii; Neopterfgii; Teleostei; Euteleostei; Neoteleostei;
                                                                                                                                                                                                                                        SPAAU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE SECURIARY, PubMed-8954766;
MEDLINE-97114AY), PubMed-8954766;
MEDLINE-97114AY), PubMed-8954766;
Cloning and expression of somatolaccin, a pituitary hormone related toning and expression of somatolaccin, a pituitary hormone related toning and prolactin from gilthead seabream, Sparus are goweth hormone and prolactin from gilthead seabream, Sparus are goweth hormone and prolactin from gilthead seabream, Sparus are goweth bornone and prolactin from gilthead seabream, Sparus are government of the seabream of the seabrea
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Ol-Oci-1996 (Rel. 34, Liast sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Somatolactin i precursor (SL).
Sparus aurata (Gilthead sea bream).
Sparus aurata (Gilthead sea bream).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelegstomi;
Acanthomorpha; Acanthopterygii; Peleostei; Euteleostei; Neoteleostei;
Ncanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
Sparidae; Sparus.
NCBI_TaxID-8175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L49205; AAA98734.1; -. HSSP; P01246; 1BST.
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P54863;
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                                                                                                                                                                                                                                                                                                                                                                                          5 LKLLLKLLKC 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . rru0103; hormone; 1.
TTS; PR00836; SOMATOTROPIN.
TTS; PS00236; SOMATOTROPIN.
TE; PS00236; SOMATOTROPIN.
TE; PS00236; SOMATOTROPIN.
TE; PS00336; SOMATOTROPIN.
TE; Glycoprotein; Signal DOTENTIAL.
10: Glycoprotein; Signal DOTENTIAL.
10: SOMATOLACTI
D 29 39 SOMATOLACTI
D 29 305 BY SIMILART
10: 145 145
145 145
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39 Bi
205 Bi
230 Bi
145 NW;
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SOMATGLACTIN 1.
SOMATGLACTIN 1.
SY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINED (GLUNAC. . .) (POTENTIAL).
67A442TD43E02364 CRC64;
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RESULT 4
SOMILSION
AC 09YGKZ
AC 09YGKZ
AC 09YGKZ
AC 09YGKZ
AC 09YGKZ
AC 09YGKZ
AC 01-MAA
DT 01-M
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Best Local S
Matches 7
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                                                        SEQUENCE PROM N.A.
TISSUS-PILLIBEARY,
MEDILINE-9910218; PubMed-9882545;
MEDILINE-9910218; PubMed-9882545;
Thu Y. Yoshiura Y., Kikuchi K., Aida K., Thomas P.;
"Cloning and phylogenetic relationship of red drum somatolactin cDNA and effects of light on plutitary somatolactin mRNA expression.";
Gen. Comp. Endocrinol. 113:69-79(1999).

TISSUS EPECIFICITY: PITUTARY GLAND.

TISSUS EPECIFICITY: PITUTARY GLAND.

TISSUS EPECIFICITY: PITUTARY GLAND.
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TISSUB-PICUITARY
CARACIA B., FUNK-STATE B., KAMAUCHI H.,
CARACIA B., FUNK-STATE B., KAMAUCHI H.,
SUBBLITTAR TOCATION: Secreted
1. SUBCELLUTAR LOCATION: SECRETED
1. TISSUB SECIFICITY: FUTUTARY GLAND.
1. TISSUB SECIFICITY: FUTUTARY GLAND.
1. SIMILARITY: BELONGS TO THE SOMMITOTROPIN/PROLACTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Somatolactin precursor (SL).
Schaenops ocellatus (Red drum).
Schaenops ocellatus (Red drum).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Peleostei; Euteleostoi; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
Schaenidae; Schaenops.
NCBI_TaxID=76340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OYVKK7;
01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Y11144; CAA72031.1; ... HSSP; P01246; IBST.
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Sparidae; Sparus.
NCBI_TaxID=8175;
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SOMATOLACTIN 2.

BY SIMILARITY.

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N-LINKED (GLCHAC...) (PO'
N-LINKED (GLCHAC...) (PO'
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Pred. No. 12;
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      231 AA
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This SWISS-PROT entry is copyright. It is produced through a collaboration

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Matches 7
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Acanthuroidei; Siganidae; Siganus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
         PROSITE;
                                                                                                modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                         Ayson F.G., de Jesus
Kawauchi H.;
                                                                                                                                                                                                                                                                                                                                                                                                                             Somatolactin precursor (SL). Siganus guttatus (Rabbitfish).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                 EMBL; AB026186; BAA83467.1; Interpro; IPRO01400; SOMATOTROPIN. Pfam; Pf00103; hormone; 1. Pfam; PF00103; hormone; 1. Pfam; PF001836; SOMATOTROPIN. PRINTS; PR00836; SOMATOTROPIN.
                                                                                                                                                                                                                                                                 "Isolation and cDNA cloning of somatolactin in rabbitfish (Siganus guttatus).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _SIGGU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00836; SOMATOTROPIN. PROSITE; PS00266; SOMATOTROPIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001400; SOMATOTROPIN. Pfam; PF00103; hormone; 1.
                                                                                                                                                                                                                                                      Submitted (APR-1999)
                                                                                                                                                                                                                                                                                                                    TISSUE-Pituitary;
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                            -18 SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
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        PS00266; SOMATOTROPIN_1;
PS00338; SOMATOTROPIN_2;
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231 /
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70.08;
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N-LINKED (GLCNAC. . .) (POT N-LINKED (GLCNAC. . .)
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Pred. No.
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12;
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ng as its content is in no
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CARBOHYD
                                                                                                                 Hormone;
SIGNAL
CHAIN
DISULFID
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-97242175; PubMed=9125164;
Cheng K.W., Chan Y.H., Chen Y.D., Y
"Sequence of a cDNA clone encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Actinopterygii; Neopterygii; Teleostei; Cypriniformes; Cyprinidae; Carassius.
                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carassius auratus (Goldfish)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997
15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                         EMBL; U72940;
HSSP; P01246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Somatolactin precursor (SL)
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                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                      Pfam; PF00103; hormone;

    -!- SUBCELLULAR LOCATION: Secreted.
    -!- SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carassius auratus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=7957;
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7; Conser
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(Rel. 35, Last sequence up
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226 NW;
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                     52.9%;
70.0%;
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70.0%;
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SOMATOLACTIN.

BY SIMILARITY.

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LY CBC5DB347C6116DC CRC64;
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SOMATOLACTIN.
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N-LINKED (GLCNAC....
Score 37; DB Pred. No. 36; 2; Mismatches
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Pred. No. 12;
3; Mismatches
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                 36;
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Euteleostei; Ostariophysi;
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somatolactin
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   1;
                                       Length 230,
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Y035_T
                                                   01-APR-1990
01-APR-1990
01-FEB-1994
                       Antigen LPMC-61
Eimeria tenella.
            Eukaryota;
                                                                                                                     EIMTE
                                                                                          LP61_EIMTE
P15714;
                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                  Complete proteome.
NP_BIND 44
                                                                                                                                                                                                                                                                                                                      Hypothetical protein; Transport;
                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE001188; AAC65030.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S. Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Y035_TREPA
083078;
16-0CT-2001
                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00005; ABC_tran;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  spirochete.";
Science 281:375-388(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98332770; PubMed=9665876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treponema pallidum.
Bacteria; Spirochaetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                       53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=160;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EM European Bioinformatics Institute. There are no restriby non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TP0034/TP0035/TP0036 FOR A METAL. PROBABLY RESPONSIBLE FOR ENERGY COUPLING TO THE TRANSPORT SYSTEM.
SUBCELLULAR LOCATION: Inner membrane-associated (Potential).
SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
                                                                                                                                                                                         LLKLLKLLK 13
                                                                                                                                                                    LVKLVLKLLK 62
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                             1990 (Rel. 14, Create
-1990 (Rel. 14, Last s
-1994 (Rel. 28, Last a
n LPMC-61 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                             TP0035;
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8; Conser
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Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;
                                                                                                                                                                                                                                                                                                                                                                 IPR001687;
                                                                                                                                                                                                                                                                                                                                                                          IPR003439; ABC_transportr
                                                                                                                                                                                                                                                                                      238 AA;
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                                                                                                    STANDARD;
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14, Last sequence up
28, Last annotation
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26460 MW;
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                                                                                                                                                                                                                               52.9%;
80.0%;
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system ATP-binding protein TP0035.
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                                                                                                                                                                                                                               Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                                 ATP
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                                                                                                                                                                                                                                                                                                                    Inner membrane; ATP-binding;
                                                             update)
                                                                                                 255 AA.
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Eukaryota; Fungi; / Saccharomycetales;

SEQUENCE FROM N.A NCBI_TaxID=4932; Saccharomyces cerevisiae (Baker's yeast)

Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetaceae; Saccharomyces.

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RESULT COPG_YEAST COPG_YEAST ID COPG_Y AC P32074 DT 01-OCT DT 16-OCT DE Coaton GN SEC21 OS Saccha OC Eukary OC Saccha OX NCBL_T RN [1]
RP SEQUEN
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Best Local
                                                                                   P32074;
01-OCT-1993 (Rel. 2
01-OCT-1996 (Rel. 3
16-OCT-2001 (Rel. 3
                                                                Coatomer gamma subunit (Gamma-coat SEC21 OR YNL287W OR N0543
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REPEAT
NON_TER
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                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M30933; AAA29079.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Identification and characterization of a target antigen of a monoclonal antibody directed against Eimeria tenella merozoites."; MOI. Biochem. Parasitol. 41:53-64(1990)
-!- FUNCTION: UNKNOWN. THE GLN-RICH TANDEM REPEATS MAY BE IMPORTANT FOR AN UNKNOWN ASPECT OF THE PARASITIC LIFE CYCLE. MAY BE AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=90348718; PubMed=2200963; Ko C., Smith C.K. II, McDonell M.;
                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=5802;
                                                                                                                                                                                                               2 KILLKLLLKLL 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: MAY BE COVALENTLY LINKED BY DISULFIDE BONDS TO OTHER POLYPEPTIDES TO FORM THE 80 kDa ANTIGEN.
DEVELOPMENTAL STAGE: PRESENT IN ALL STAGES THROUGHOUT THE SPORULATION OF THE OOCYSTS AND IN THE SPOROZOITES FOLLOWING
                                                                                                                                                                                            RLLLKLLLLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A60637;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMPORTANT IMMUNOGEN
                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sporozoite;
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                                                                                                                                    STANDARD;
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31267 .MW;
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57
65
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90
103
140
152
164
172
192
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sporulation.
                                                                                                                                                                                                                                                                                         8C5E6005FFFC2DB3 CRC64;
                                                                                                                                                                                                                                               39;
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                                                                        (Gamma-COP)
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                                                                                                                                                                                                                                                       Length 255;
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Best Local S
Matches 7
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01-JAN-1988
16-OCT-2001
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                                                                                                              Bacillus subtilis.
Bacteria; Firmicutes; Ba
Bacillus/Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002553; Adaptin_N.
Pfam; PF01602; Adaptin_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M59708; AAA34598.1; -.
EMBL; Z71563; CAA96204.1; -.
PIR; A33151; A33151.
PIR; S28915; S28915.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hosobuchi M.M., Kreis T., Schekman "SEC21 is a gene required for ER to encodes a subunit of a yeast coator
MEDLINE-88260878; PubMed-2838724; Perego M., Hoch J.A.; Pschlation and sequence of the sp sporulation in Bacillus subtilis.
                                                                                                                                                                        Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transport; Protein transport; Golgi stack; Membrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAY-1996) to the -i- FUNCTION: THE COATOMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glansdorff N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Messenguy F., Dubois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM
                                                          STRAIN-168;
                                                                      SEQUENCE FROM
                                                                                                                                                                                                                                   P06630;
                                                                                                                                                                                                                                                EAG_BACSU
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                                                                                                  NCBI_TaxID=1423;
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                                                                                                                                                                                                                                                                                                                                                1 CKLLLKLLKLL 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EÚNCTIÓN: THE CÓATOMER IS A CYTOSOLIC PROTEIN COMPLEX THAT BINDS
TO DILYSINE MOTIFS AND REVERSIBLY ASSOCIATES WITH GOLGI NON-
CLATHRIN-COATED VESICLES, WHICH FURTHER MEDIATE BIOSVINHETIC
PROTEIN TRANSPORT FROM THE ER, VIA THE GOLGI UP TO THE TRANS GOLG
NETWORK. COATOMER COMPLEX IS REQUIRED FOR BUDDING FROM GOLGI
MEMBRANES, AND IS ESSENTIAL FOR THE RETROGRADE GOLGI-TO-ER
TRANSPORT OF DILYSINE-TAGGED PROTEINS (BY SIMILARITY).
SUBUNIT: OLIGOMERIC COMPLEX THAT CONSISTS OF AT LEAST THE ALPHA,
BETA, BETA, GAMMA, DELTA, EPSILON AND ZETA SUBUNITS.
SUBCELLULAR LOCATION: THE COATOMER IS CYTOPLASMIC OR POLYMERIZED
ON THE CYTOPLASMIC SIDE OF THE GOLGI, AS WELL AS ON THE
VESICLES/BUDS ORIGINATING FROM IT (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE COPG FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                            Similarity 7; Conser
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935 AA;
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1 16.4
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kDa
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104830 MW; 99DC7D737D4EF761 CRC64;
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                                                                                                                                                                     Last sequence update)
Last annotation update)
protein in SPOOE 3'region.
                                                                                                                                                                                                                    Created)
                                                                                                                Bacillus/Clostridium group; s group; Bacillus.
 of the spoOE gene: subtilis.";
                                                                                                                                                                                                                                                                                                                                                                         Score 37; DB Pred. No. 1.3e 3; Mismatches
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coatomer.";
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              its
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              role
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RESULT 11
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                                                                                        PROSITE; PROSITE;
                                                                                                                                                                                                                                                                                                  This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Somatolactin precursor (SL).

Hippoglossus hippoglossus (Atlantic halibut).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;

Pleuronectoidei; Pleuronectidae; Hippoglossus.

NCBI_TaxID-8267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein; Sporulation; Complete proteome. SEQUENCE 143 AA; 16429 MW; D7410B50963D7A75 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Y00526; CAA68584.1;
EMBL; Z99111; CAB13238.1;
PIR; S03747; S03747.
SubtiList; BG10770; eag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                           raqi F., Gong Z., Hew C.L., Crim L.W.;
"Isolation and characterization of somatolactin genes from tw
water marine teleosts, lumpfish (Cyclopterus lumpus) and hali
(Hippoglossus hippoglossus).";
Mol. Mar. Biol. Biotechnol. 2:96-103(1993).
-i- SUBCELIJULAR LOCATION: Secreted.
-i- SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P45641;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=93372995; PubMed=7689905;
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                                                                                                                                                                EMBL; L02117; HSSP; P01246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mol. Microbiol. 1:125-132(1987).
                                                                           dormone;
                                                                                                                       PRINTS; PR00836;
                                                                                                                                                                                                                                                                                     between
                                                                                                                                                   [nterPro; IPR001400; SOMATOTROPIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 LLLKMLLRFIK 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
hes 7; Conserv
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                                                                                                                                      PF00103;
                                                                                     PS00266; SOMATOTROPIN_1;
PS00338; SOMATOTROPIN_2;
                                                                           Glycoprotein;
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   24
28
88
221
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                                                                                                                                                                              AAC38003.1;
                                                                                                                     hormone; 1.
6; SOMATOTROPIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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Pred. No.
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There are no restrictions on
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and halibut
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MBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                   senegalensis).";
Gene 147:227-230(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Solea senegalensis (Sole).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei
Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
Soleoidei; Soleidae; Solea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence up
01-NOV-1997 (Rel. 35, Last annotation
                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-95011619; PubMed-7926805;
Pendon C., Martinez-Barbera J.P., Valdivia M.M.;
"Cloning of a somatolactin-encoding cDNA from so senegalensis).":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Somatolactin precursor (SL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P45642;
01-NOV-1995 (Rel.
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                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                    Pfam; PF00103; hormone;
                                                                                                                                                                                                                                                         EMBL; U06753;
HSSP; P01246;
                                                                                                                                                                                                                                                                                                                 modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                       Hormone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=28829;
                                                                                                                                                                                                                                                InterPro; IPR001400; SOMATOTROPIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            212
212
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TISSUE SPECIFICITY: PITUITARY GLAND.
SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
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                    LKLLLKLLKC
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6; Conser
                                                                                                                                                                                                                          PR00836; SOMATOTROPIN.
                                                     Similarity
                                                                                                                                                                                       Glycoprotein;
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144
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SOMATOTROPIN_2;
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SOMATOLACTIN.
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BY SIMILARITY.
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N-LINKED (GLCNAC. . .) (PO'

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N-LINKED (GLCNAC. . .) (PO'
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Pred.
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1E3C16622F75946A CRC64;
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RESULT 13

SOML_PAROL STANDARD

ID SOML_PAROL STANDARD

AC P20362;

DT 01-FEB-1991 (Rel. 17, C

DT 01-FBB-1991 (Rel. 17, L

DT 01-NOV-1995 (Rel. 32, L
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PRR1_BOVIN
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Matches 6
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01-NOV-1988
01-NOV-1997
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Somatolactin precursor (SL).

Paralichthys olivaceus (Flounder).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;

Pleuronectoidei; Paralichthyidae; Paralichthys.
                                                                                                                                                                                                                                                                              SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                                                                       EMBL; M33696; AAA49445.1; -.
EMBL; M33695; AAA49444.1; -.
PIR; A35793; A35793.
HSSP; P01246; 1BST.
                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the
                                             P05402;
                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kawauchi H.;
"cDNA cloning of somatolactin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ono M., Takayama Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Pituitary;
MEDLINE=90272707;
                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00103; hormone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hormone and prolactin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=8255;
                                                          PRR1_BOVIN
                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00836; SOMATOTROPIN
                                                                                                                                                                                                                                                                                                     Hormone;
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                                                                                                                                      5 LKLLLKLLKC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE SPECIFICITY: PITUITARY GLAND. SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION:
                                                                                                                  MEIFLKLLKC
                                                                                                                                                             Similarity 60.06; Conservative
                                                                                                                                                                                                                                                                                                               PS00266;
PS00338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FROM N.A.,
                                                                                                                                                                                                                                                                                                      Glycoprotein;
88 (Rel. 09, Created)
88 (Rel. 09, Last sequence update)
97 (Rel. 35, Last annotation update)
prolactin-related protein I precursor
                                                                                                                                                                                                                                                                                                                                                            IPR001400; SOMATOTROPIN.
                                                                                                                                                                                                                                             25
29
89
222
                                                          STANDARD;
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                                                                                                                                                                                                                                                                                                               SOMATOTROPIN_1;
SOMATOTROPIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=2349240;
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N-LINKED (GLCNAC...
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                                                                                                                                                              Score 36; DB Pred. No. 52; 3; Mismatches
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                                                            238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Usage
                                                                                                                                                                                     Length 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yasunaga T., Noso T.,
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                                                                                                                                                                                                                        CRC64;
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EMBL; M25494; AAA30727.1; -JOIN
EMBL; M25491; AAA30727.1; JOIN
EMBL; M25492; AAA30727.1; JOIN
EMBL; M25492; AAA30727.1; JOIN
EMBL; M25493; AAA30727.1; JOIN
FIR; A31417; A31417.
HSSP; Q28632; IAN3.
                                                                   01-FEB-1996
01-FEB-1996
16-OCT-2001
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CONFLICT
SEQUENCE
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MEDLINE-87289662; PubMed-3475696;
Schuler L.A., Hurley W.L.;
"Molecular cloning of a prolactin placenta.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ebbitt D.M., Hurley W.L., Kessler M.A., McDonald D.J., Schuler L.A.; "Characterization of the gene corresponding to bovine placental prolactin-related cDNA I: evolutionary implications."; DNA 8:161-169(1989).

-I- FUNCTION: PLACENTAL PROLACTIN-RELATED PROTEINS MAY PLAY A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                         Hypothetical MG147.
                                                                                                                                      Y147_MYCGE
P47393;
                                                                                                                                                                                     MYCGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9913;
[1]
Mycoplasma genitalium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00836; SOMATOTROPIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 formone;
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                                                                                                                                                                                                                                                                           21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: PLACENTAL PROLACTIN-RELATED PROTEINS MAY PLAY SPECIFIC ROLE DURING GESTATION. SUBCELLULAR LOCATION: Secreted.
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STRAIN-ATCC 33530 / G-37;
MEDLINE-96026346; PubMed-7569993;
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O94m45 streptococc
O9vug7 drosophila
O928r1 chlamydia p
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ALIGNMENTS

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Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T., Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D., Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A., Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K., Celniker S., Rubin G.M.;

"An exploration of the sequence of a 2.9-Mb region of the genome of Drosophila melanogaster: the Adh region.";

Genetics 153:179-219(1999).
                              SEQUENCE FROM N.A.

STRAIN-Y, AND CN BW SP;

Celniker S.E., Abbayani A., Arcaina T.T., Baxter E., Blazej R.G.,

Butenhoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.

Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,

HOUSTON K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,

Lewis S., Li P., Lomotan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,

Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequelra A.,

Sethi H., Snir E., Svirskas R.R., Wan K.H., Weinburg T., Zhang R.,

Zieran L.L., Rubin G.M.,
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 144 0 KDA PROTEIN (RK GENE PRODUCT).
RK OR BG:DS00180.13 OR CG8930.
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STRAIN-Y, AND CN BW SP;
MEDLINE-99403001; PubMed-10471707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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PRINTS; PR00237; GPCRRHODDPSN.
SMART; SM00370; LRR; TYP; 4.
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InterPro; IPR003591; LrR_typ.
InterPro; IPR003591; LrR_typ.
InterPro; IPR003591; LrR_typ.
Pfam; PF00001; 7tm_1: 1.
PRINTS; PR000237; GPCRHODOPSN.
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01-DEC-2001
01-DEC-2001
                                                                                                                  Submitted (JAN-2001) to the EMBL; AJ302074; CAC48100.1; Hypothetical protein. SEQUENCE 295 AA; 32657 MY
                                                                                                                                                   Obregon V., Garcia P., Garcia E., Lopez R., Garcia J.L.; "Complete nucleotide sequence and analysis of the temperate bacteriophage MM1 genome of Streptococcus pneumoniae."; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                            SEQUENCE FROM N.A. Obregon V., Garcia P.,
                                                                                                                                                                                                                                             Viruses; dSDNA viruses, no RNA stage; Caud
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01-DEC-2001 (TrEMBLrel. 19, La
01-DEC-2001 (TrEMBLrel. 19, La
01-DEC-2001 (TrEMBLrel. 19, La
HYPOTHETICAL 32.7 KDA PROTEIN.
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STRAIN=CANTON S.; TISSUE=WHOLE ANIMAL;
STRAIN=20359836; PubMed=10899142;
MEDLINE=20359836; PubMed=10899142;
MEDLINE=20359836; PubMed=10899142;
                                                                                                                                                                                                                                    NCBI_TaxID=120574;
                                                                                                                                                                                                                                                                                                                                             Q94M45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Molecular Cloning, Genomic Organization, Developmental Regulation, and a Knock-Out Mutant of a Novel Leu-Rich Repeats-Containing G Protein-Coupled Receptor (DLGR-2) from Drosophila melanogaster.";
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Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome Res. 10:924-938(2000).
EMBL; AF142343; AAF66608.1; -.
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Pred. No. 88;
2; Mismatches
                                                             Pred.
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                                                  Mismatches
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Ballew R.M., Basu A., Baxedale J., Bayaktaroglu L., Belakin D.,
RA Ballew R.M., Basu A., Baxedale J., Bayaktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beleson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Berson K.Y., Brands D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cowley S., Dahlke C., Davenport L., Davess P.,
RA Ge Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Ge Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Durbin K.J., Evangelista C.G., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Sheel H.,
RA Shie B.C., Siden K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Shie B.C., Siden K.A., Nixon K., Nusskern D.R., Sheeler F., Shen H.,
RA Shie B.C., Siden K.A., Nixon K., Shupski M.P., Smith T.,
RA Sheng X.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Jehng X.H., Zhong F.N., Zhong W., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Jehng X.H., Zhong F.N., Zhong W., Zhan M., Zhang G., Zhao Q., Zheng L.,
Solence 287.2165-2195(2000)
D. Ra Kang R., Sheng R., Sheng R., Sheng L.,
Sheng R., Sheng R., Sheng R., Sheng R., Sheng L.,
Sheng R., She
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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12193 MW;
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46.2%;
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01-DEC-2001 (TIEMBLrel. 10, Last sequence update)
01-DEC-2001 (TIEMBLRel. 19, Last annotation update)
HYPOTHETICAL 18.2 KDA PROTEIN.
CPN0277 OR CPJ0277 OR CPJ0277 OR CPJ0277
                                                                                                                                                      Q9PSN4;
01-MAY-2000 (
01-MAY-2000 (
01-DEC-2001 (
SEQUENCE.
MEDLING-95291367; PubMed=7773329;
                                                               Actinopterygii; Neopterygii; Teleostei; Acanthomorpha; Acanthopterygii; Percomorparidae; Sparus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20150255; PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg
Eisen J., Fraser C.M.;
"Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
pneumoniae AR39.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; "Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Olinger L., Grimwood J., Davis R.W., Stephens R.S.; "Comparative genomes of Chlamydia pneumoniae and C. trachomatis."; Nat. Genet. 21:385-389(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99206606; PubMed=10192388;
Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
                                                                                                                             Sparus aurata (Gilthead sea
                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein; Complete SEQUENCE 169 AA; 18203 MW;
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila
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                                                                                                                                                                                                          Q9PSN4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20330349; PubMed=10871362; Shirai M., Hirakawa H., Kimoto M.,
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AE0001613; AAD18426.1; -.
AE002208; AAF38311.1; -.
AP002546; BAA98487.1; -.
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50.0%;
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Pred. No.
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4A3B2967C18A7424 CRC64;
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                                                                                       Percomorpha;
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                                                                                     Vertebrata; Euteleostomi;
Euteleostei; Neoteleostei;
rpha; Perciformes; Percoide
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01-NOV-1996 (TrEMBLrel. 01, L
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CHROMOSOME XII COSMID 8003.
YLR283W OR L8003.9.
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Eukaryota; Metazoa; Chordata; Craniata; Verte
Actinopterygii; Neopterygii; Teleostei; Eutel
Acanthomorpha; Acanthopterygii; Percomorpha;
Moronidae; Dicentrarchus.
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                                                                                                                                                                                                                                                            PRINTS; PR00836;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SOMATOLACTIN PRECURSOR (FRAGMENT).
                                                                                                                 198
                                                                                                                                                                                                                                                               interPro: IPR001400; SOMATOTROPIN fam; PF00103; hormone; 1
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=13489;
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01-MAR-2001
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PRINTS; PR00836; SOMATOTRODIN.

PROSTTE; PS00266; SOMATOTROPIN_1; 1.

PROSITE; PS00338; SOMATOTROPIN_2; 1.

SEQUENCE 207 AA; 23888 MW; FDA8B;
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HSSP; P01241; 1AXI
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AJ277390; CAC16116.1; -.
P01241; 1AXI.
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                                                                                                                                                 Similarity 70.07; Conservative
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                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           novel pituitary protein: isolation from Sparus aurata.";
Biotechnol. 4:117-122(1995).
                                                                                                                                                          57.1%;
70.0%;
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70.0%;
                                                                                                                                                                                                 MW;
                      Created)
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Pred. No. 39;
3; Mismatches
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                                                                                                                                                                                            POTENTIAL.
SOMATOLACTIN.
; 95CBB324A6069F00 CRC64;
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Pred. No. 38;
3; Mismatches
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Euteleostei; Neoteleostei;
rpha; Perciformes; Percoidei;
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ea bass (Dicentrarchus
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MEDLINE-97313267; PubMed-9169871;
A Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansorge Johnston M., Hillier L., Riles L., Dubois E., Dusterhoft A., Andre B., Dehius H., Dubois E., Dusterhoft A., Entian K.D., Floeth M., Goffeau A., Hebling U., Heumann K., Andrews H., Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Kotter P., Andrews H. W., Miosga T., Mostl D., Andrews H. W., Miosga T., Mostl D., Muller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M., Moller-Auer S., Nentwich U., Obermaier B., Firavandi E., Pohl T.M., Portetelle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Rose M., Scharfe M., Werhasselt P., Underwood A.P., Urrestarazu L.A., Vandenbol M., Verhasselt P., Underwood A.P., Urrestarazu L.A., Vandenbol M., Verhasselt P., Underwood M. P., Urrestarazu L.A., Vandenbol M., Wendler H., Zalmmermann F.K., Zollner A., Hani J., Hohelsel J.D., Wender M., Wender M., Wendler M., Wender M., We
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Shake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9CUE5 PRELIMINARY; PRT; 756 AA.
Q9CUE5;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
4931427F14RIK PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                    STRAIN-C57BL/6J; TISSUE=TESTIS; MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=C57BL/6J; T
                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4931427F14RIK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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NCBI_TaxID=4932;
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58.3%;
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Pred. No. 54;
4; Mismatches
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Sciurognathi; Muridae;
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                                                                                                                                                    Ishii Y.,
Fukuda S.,
manaka I.,
Saito R.,
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01-OCT-2000
01-OCT-2000
01-DEC-2001
                               Q9FL22; PRELIMINARY; PRT; 1022 AA.
Q9FL22; Q1-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
GENOMIC DNA, CHROMOSOME 5, P1 CLOME.WPLI2.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; endicotyledons; core endicots; Rosid eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hall N., Bowman S., Quail M., Ivens A.C., Kay Lennard N.J., Clark L.N., Harris B.R., Melvill Gerrard C., Rajandream M.A., Barrell B.G.; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ EMBL; AL359782; CAB95541.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro; IPRO00847; HTH_Lysr.
PROSITE; PS00044; HTH_LYSR_FAMILY; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 988 AA; 107318 MW; EFB3A38C56AE6
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Eukaryota; Euglenozoa;
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"Functional annotation of a Nature 409:685-690(2001).
EMBL; AK016477; BAB30259.1;
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Suzuki H., Toyo-oka K., Wang K.
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eurosids II; Brassicales; NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 69.: 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 756 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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86030 MW;
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69.2%;
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61.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         full-length mouse
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 1.404; Mismatches
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l; Mismatches
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No. 1.4e+02;
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Melville
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Best L
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                                Pfam; PF00041; fn3; 4.
Pfam; PF00047; f9; 6.
Pfam; PF000014; FNTYPEIII.
SMART; SM00060; FN3; 4.
SMART; SM00408; IGC2; 4.
SMART; SM00410; IG_like; 2.
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01-JAN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDLINE-92198663; PubMed-1550678;

Johansen K.M., Kopp D.M., Jellies J., Johansen J.;

"Tract formation and axon fasciculation of molecularly distinct peripheral neuron subpopulations during leech embryogenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hirudo medicinalis (Medicinal leech).
Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida;
Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kaneko T., Kotani
Tabata S.;
                                                                                                                                                                                                                                                                                     J. Cell Biol. 138:143-157
EMBL; U92813; AAC47654.1;
HSSP; P20241; 1CFB.
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SEQUENCE FROM
                                                                                                                                                                                                                                            InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                       Huang Y., Jellies J., Johansen "Differential glycosylation of
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE-97362067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neuron
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                                                                                                                                                                  InterPro;
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                                                                                                                                                                                                                                                                                                                                                   formation.";
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                     lobulin
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8; Conserv
                                                                                                                                                                                 IPR003598;
IPR003600;
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IPR003962; FnIII_rep
IPR003961; FN_III.
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1 (TrEMBLrel. 19,
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                     domain;
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No. 1.5e+02;
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and LeechCAM,
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Query Match Best Local S Matches

Similarity 9; Conserv

Conservative

57.1%;

Score 40; DB Pred. No. 2.4e 1; Mismatches

DB 5; ... 2.4e+02;

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Best Local :
SEQUENCE: STRAIN-CV. COLUMBIA;

STRAIN-CV. COLUMBIA;

Sakano H., Liu S.X., Yu G., Lee J., Lenz C., Pham P., Toriu
Chin C., Chiou J., Choi E., Chung M., Gonzalez A., Howng B
Vaysberg M., Altafi H., Brooks S., Buehler E., Chao Q., Co
Conway A. B., Hansen N.F., Johnson-Hopson C., Khan S., Kim
Miranda M., Nguyen M., Palm C., Shinn P., Southwick A., Da
Ecker J.R., Federspiel N.A., Theologis A.;
"The sequence of BAC F2J10 from Arabidopsis thaliana chrom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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InterPro; IFR003152; FATC.
InterPro; IFR003152; FATC.
InterPro; IFR003403; FI3_PI4_kinase.
Pfam; PF02259; FATC; 1.
Pfam; PF002560; FATC; 1.
Pfam; PF00454; PT3_PI4_kinase; 1.
SMART; SM00146; PT3_FI4_kinase; 1.
SMART; SM00146; PT3_FT4_kINASE_1; 1.
PROSITE; PS00290; PT3_4_KINASE_3; 1.
SEQUENCE 2481 AA; 279187 MW; DA6631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9LPM4;
01-OCT-2000 (
01-OCT-2000 (
01-DEC-2001 (
                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F2J10.
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01-MAR-2001
01-DEC-2001
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eueurosids_I; Brassicales; Brassicaceae; Arabidopsis.
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(im C., Lar
                                                                                                             Davis
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                                                                                                      Lam B., R.W.,
                                                                                                                                                                                               Liu A.,
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Q9ZT73
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InterPro; IPRO03152; FATC.
InterPro; IPRO03403; PI3_PI4_kinase.
Pfam; PF02259; FATC; 1.
Pfam; PF02259; FATC; 1.
Pfam; PF00254; PI3_PI4_kinase; 1.
PFAm; PF00454; PI3_PI4_kinase; 1.
PROSITE; PS00915; PI3_4_KINASE_1; 1.
PROSITE; PS00916; PI3_4_KINASE_2; 1.
PROSITE; PS00916; PI3_4_KINASE_3; 1.
SEQUENCE 2513 AA; 282911 MW; A4F
                                                                                                                                                                                                                                                                                                    PROSITE; PS50297; ANK_REP_REGION;
ANK repeat; Hypothetical protein;
SEQUENCE 641 AA; 70466 MW; ECI
                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002110; ANK. Pfam; PF00023; ank; 9. SMART; SM00248; ANK; 2.
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Submitted (MAR-2000) to the EM
EMBL; AF071527; AAD11587.1; -
EMBL; AL161496; CAB77830.1; -
                           304
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Huang E.N., Parnell L.D., de la E
Dedhia N.N., McCombie W.R.;
"Genomic sequence of Arabidopsis
18.8 cm.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheopsisermatophyta; Magnoliophyta; eudicotyledons; core eudicots; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-MAY-1999 (TIEMBLIEL 10, La
01-DEC-2001 (TIEMBLIEL 19, La
HYPOTHETICAL 70.5 KDA PROTEIN.
F9H3.7 OR AT4G03450.
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                                                                            5 LKLLLKLLKC 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    797 LLLGLLLKLLK 807
* VKIFLKLLKC
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                                                                                                                                                  Similarity 7; Conser
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                                                                                                                                              Conservative
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udicots; Rosidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence:
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seq
   Issued_Patents_AA:*
1: /cgn2_6/ptodata/2,
2: //gn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: //gn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
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length: 2000000000
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Match Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenCore version
Copyright (c) 1993 - 2000
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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    24425594 residues
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          US-09-000-692-1
US-08-569-188-8
PCT-US94-07019-1
US-08-569-188-10
US-08-569-188-12
PCT-US94-07019-11
PCT-US94-07019-11
PCT-US94-07019-11
PCT-US94-07019-12
US-08-569-188-3
US-08-569-188-3
US-08-818-252-3
US-08-818-252-3
US-08-818-252-3
US-08-918-5
PCT-US94-07019-5
US-07-725-331-60
PCT-US91-05047-61
US-07-725-331-62
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US-07-725-331-63
PCT-US91-05047-63
US-07-725-331-63
PCT-US91-05047-63
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Sequence 1, Appli
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37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	38
52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	54.3
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PÇT-US94-07019-15	PCT-US94-07019-6	us-09-296-089-36	US-08-958-993A-12	US-08-960-054A-12	US-08-569-188-15	US-08-569-188-6	PCT-US94-07019-14	PCT-US94-07019-4	US-08-569-188-14	US-08-569-188-4	PCT-US94-07019-13	PCT-US94-07019-2	US-08-569-188-13	US-08-569-188-2	PCT-US91-05047-1	US-07-725-331-1	US-08-944-133-13
15,	Sequence 6, Appli	Sequence 36, Appl	Sequence 12, Appl	•	Sequence 15, Appl	Sequence 6, Appli	Sequence 14, Appl	Sequence 4, Appli	Sequence 14, Appl	Sequence 4, Appli	Sequence 13, Appl	Sequence 2, Appli	Sequence 13, Appl	Sequence 2, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 13, Appl

ALIGNMENTS

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RESULT 2
US-08-569-188-8
; Sequence 8, Application US/08569188
; Sequence 10. 5847047
; Patent No. 5847047
; GENERAL INFORMATION: NOVEL ANTIMICORBIAL COMPOSITIONS
; TITLE OF INVENTION: NOVEL ANTIMICORBIAL COMPOSITIONS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS: 1
; ADDRESSEE E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/000,692
CURRENT FILING DATE: 1997-12-30
EARLIER APPLICATION NUMBER: 08/778657
EARLIER FILING DATE: 1997-01-03
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PATENTIN VEY: 2.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application Patent No. 6339067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 20
TYPE: PRT
ORGANISM: Unknown
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SLATTUM, PAUL M
APPLICANT: HANSON, LISA J
TITLE OF INVENTION: A PROCESS OF MAKING A COMPOUND
TITLE OF INVENTION: FROM A TEMPLATE DRUG
FILE REFERENCE: TPCIP000692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: WOLFF, JON A
APPLICANT: HAGSTROM, JAMES E
APPLICANT: BUDKER, VLADIMIR G
APPLICANT: TRUBETSKOY, VLADIMIR S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Unknown Organism: AMPHIPATHIC
                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 12; Conserv
                                                                                                                                                                                                                                                                                             1 CKLLKKLLKLWKKLLKKLKC
                                                                                                                                                                                                                                                                                                              1 CKLLLKL-----LLKLLKC
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); Mismatches
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No.
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COUNTRY:

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TITLE OF INVENTION: NOVEL ANTIMICROBIAL
NUMBER OF INVENTION: COMPOSITIONS
COMPUTER READANCES: 1500SITIONS
COMPUTER READANCES: 1500SITIONS
COMPUTER: MACINTOSH
COMPUTER: MICROSOTY MORD, 4.0
APPLICATION NUMBER: PCT/US94/07019
APPLICATION SOME 22, 1993, 852
ENGRY CHARACTERIZICS:
STEANUBENESS: UNKOWN
PCT-US94-07019-8
PET-US94-07019-8
PET-US94-07019-8
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CILLING DATE:
CILLING DATE:
CILLING DATE:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNBER: 08/082/852
APPLICATION UNBER: 08/082/852
APPLICATION NUBBER: 08/082/852
APPLICATION NUBBER: 08/082/852
APPLICATION AFFORMATION:
ATTORNEY APPLICATION ANAMETHY
FINANCE LANGUAGE TO NUBBER: COPE
FELICAMONICATION TWOMBER: COP-29
TELEPHONE: 302-792-8112
INFORMATION: 302-79-0164
LENGTH: 14 amino acids
TOPOLOGY:
SEDIENCE CHARACTED ID
NOLECULE TYPE: unknown
US-08-569-188-8 peptide

F7 18-8 peptide
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**DED: TO NUM. 
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Best Local Similarity
Matches 10; Conservative
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OPERATING SYSTEM.
SOFTWARE: BM PC COMPATIBLE
CURRENT APPLICATION MICROSOFT WINDOWS 95
PILICATION NUMBER: US/08/560 100
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OF THE COMPATIBLE OF THE COMPATIBLE OF THE CAPTURE OF THE COMPATIBLE OF THE COMPATI
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MEDIUM TYPE: DISKETT
                                                                                                                                                                                                                   57.1%, Score 40; DB 5; Length 14;
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US-08-569-188-10
Sequence 10, Application US/08569188
Fatent No. 5847047
GENERAL INFORMATION:
SERVICANT: SHARON LPRETTA HAYNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
PRIASSIFICATION: 525
APPLICATION: 525
APPLICATION BATA.
APPLICATION BATA.
APPLICATION WINBER: 08/082.852
REGISTRATION ALMOSTHY FLOYD
REPERCE/DOCKET NUMBER: 30.692
TELEPHONE: 30.2-7992-8112
INFORMATION SOUTHER: CR-92:
INFORMATION SOUTHBER: CR-92:
INFORMATION SOUTHBER: CR-92:
INFORMATION AND INFORMATION: 30.2-7992-8112
INFORMATION FOR SEO ID NO.
INFORMATION FOR SEO ID NO.
INGTH: 18 ACTERISTICS: 1:
TYPE: amino acid acids
TOPOLOGY: unknown
US-08-569-188-1
PRICASSIS Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Дb
                               COUNTRY: UN
ZIP 19898
                                                               APPLICANY: SHALL,
TITLE OF INVENTION: LPRETTA HAYNIE
OF INVENTION: NOVEL ANTIMICORBIAL COMPOSITIONS
ADDESSIBE: E. I. DU PONT DE NEMOURS AND COMPANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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APPLICANT: SHARON LPRETTA HAYNIE
TITLE OF INVENTION: NOVEL ANTINICORBIAL COMPOSITIONS
CORRESPONDENCE ADDRESS: 18
ADDRESSES: E. T. DU PONT DE NEMOURS AND COMPOSITIONS
STREET: 1007 MARKET STREET
WILMLINGTON
COUNTRY: INTITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
US-08-569-188-1
Sequence 1, Ar
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83.38;
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8-6104-02018-8

Query Match Best Local Similarity 57.1 Matches 10: Conservative

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COMPUTER READABLE FORM:

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Вb
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US-08-569-188-11
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Best Local Similarity
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ETILING DATE: JUNE 22, 1993
ATTORNEY/AGENT INFORMATION:
NAME: LINDA AXAMETHY FLOYD
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CR-9295-A
TELECHMONICATION INFORMATION:
TELEPHONE: 302-892-8112
TELEFAX: 302-773-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
CLASSIFICATION: 525
PRIOR APPLICATION NUMBER: 08/082,85:
APPLICATION NUMBER: 08/082,85:
FILING DATE: JUNE 22, 1993
ATTORNEY/AGENT INFORMATION:
NAME: LINDA AXAMETHY FLOYD
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CR-9
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY STREET: 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: SHARON LPRETTA HAYNTE
TITLE OF INVENTION: NOVEL ANTIMICORBIAL COMPOSITIONS
NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 525
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD FOR WINDOWS 95 (7.0)
                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1007 MARI
CITY: WILMINGTON
STATE: DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/569,188 FILING DATE:
                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
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IBM PC COMPATIBLE
SYSTEM: MICROSOFT WINDOWS 95
MICROSOFT WORD FOR WINDOWS 95 (7.0)
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83.3%;
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Pred. No. 4.3;
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Best Local Similarity
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Best Local S
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                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                            NAME: LINDA AXAMETHY FLOYD
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CR
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD FOR WINDOWS 95 (7.0)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: SHARON LPRETTA HAYNIE
TITLE OF INVENTION: NOVEL ANTIMICORBIAL COMPOSITIONS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/0 FILING DATE: JUNE 22, 19 ATTORNEY/AGENT INFORMATION: NAME: LINDA AXAMETHY FLO
                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 525
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                         MOLECULE TYPE:
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TOPOLOGY: unl
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KKLLKLLKKLLK 15
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1007 MARKET STREET
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302-773-0164
                                                             Conservative
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83.3%;
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Pred. No. 4.3;
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Pred. No. 4.3;
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RESULT 8 PCT-US94-07019-1

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Sequence 1, Application PC/TUS9407019 GENERAL INFORMATION:

NOVEL ANTIMICROBIAL COMPOSITIONS

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                               Qy
                                                                                                                                  TOPOLOGY: unknown

MOLECULE TYPE: peptide
PCT-US94-07019-10
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PCT-US94-07019-10
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APPLICANT:
TITLE OF INVENTION: NOVEL AND TITLE OF INVENTION: COMPOSITION OF SEQUENCES: 15
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: MACINTOSH
COMPUTER: MACINTOSH
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                                                          Best Local Similarity Matches 10; Conserv
                                                                                        Query Match
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                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US94/O:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/082,852
FILING DATE: JUNE 22, 1993
INFORMATION FOR SEQ ID NO: 10:
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Best Local
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LENGTH: 16 amino acids
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FILING DATE: JUNE 22, 1993
INFORMATION FOR SEQ ID NO: 1:
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MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
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LENGTH: 16 amino acids
TYPE: amino acid
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OPERATING SYSTEM: MACINTOSH 6.0
SOFTWARE: MICROSOFT WORD, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/070
PRIOR APPLICATION DATA:
                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: unl
4 KKLLKLLKKLLK 15
                          2 KILLKLLKILK 13
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TOPOLOGY: un!
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Pred. No. 4.3;
0; Mismatches
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Pred. No. 4.3;
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RESULT

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APPLICATION NUMBER: 08/082,8
FILING DATE: JUNE 22, 1993
INFORMATION FOR SEQ ID NO: 12:
SEQUIENCE CHARACTERISTICS:
LENGTH: 16 amino acids
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PCT-US94-07019-12
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APPLICATION NUMBER: 08/082,852
FILING DATE: JUNE 22, 1993
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
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Best Local Similarity
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                                                                                                                                          MOLECULE TYPE:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: MACINTOSH 6.0 SOFTWARE: MICROSOFT WORD, 4.0 CURRENT APPLICATION DATA:
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TOPOLOGY: unk
MOLECULE TYPE:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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MEDIUM TYPE: FLOPPY
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OPERATING SYSTEM: MACINTOSH 6.0
SOFTWARE: MICROSOFT WORD, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07
                                                  Local Similarity 83.
                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: unl
                                                                                                                                                      TOPOLOGY:
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MEDIUM TYPE: FLOPPY DISK
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                        2 KLLIKILKILK 13
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4 KKLLKLLKKLLK 15
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MACINTOSH
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83.3%;
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                                                  0; Mismatches
                                                            Score 40; DB 5;
Pred. No. 4.3;
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Pred. No. 4.3;
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                                                                                                                                                                                                                                             Patent No. 5998204
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                             Sequence 39, Application US/08818253
                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Patent No. 5847047
GENERAL INFORMATION:
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-08-569-188-3
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                                                                                                                                                      APPLICANT: Tsien, Roger Y.
APPLICANT: Miyawaki, Acsushi
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: DETECTION OF ANALYTES
NUMBER OF SEQUENCES: 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: ui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: LINDA AXAMETHY FLOYD
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CR-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08
FILING DATE: JUNE 22,
                COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                          ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: SHARON LPRETTA HAYNIE
TITLE OF INVENTION: NOVEL ANTIMICORBIAL COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
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OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD FOR WINDOWS 95 (7.0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1007 MAKE
CITY: WILMINGTON
                                                                                              COUNTRY: U
                                                 COUNTRY: UZIP: 92037
                                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
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 COMPUTER:
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                                                              USA
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IBM Compatible
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83.3%;
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                                                                                                            Square, Suite 1400
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                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 17;
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PCT-US94-07019-3

Sequence 3, Application PC/TUS9407019 GENERAL INFORMATION:

TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES:

NOVEL ANTIMICROBIAL COMPOSITIONS
15

APPLICANT:

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                                                                                                                                                                                  ; OTHER INFORMATION: Calmodulin binding peptide-2 US-08-818-252-39
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                                                                                           Query Match
Best Local Similarity
Whes 10; Conserv.
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RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-818-252-39
                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 39
LENGTH: 17
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 39, Application US/08818252B Patent No. 6197928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                         APPLICANT: Tsien, Roger Y.
APPLICANT: Miyawaki, Atsushi
APPLICANT: Miyawaki, Atsushi
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: DETECTION OF ANALYTES
FILE REFERENCE: 07257/042001
CURRENT FILLNG DATE: 1997-03-14
NUMBER OF SEQ ID NOS: 56
NUMBER OF SEQ ID NOS: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 619/678-507
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                   ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 14-MAR-1997 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Haile, Ph.D., Lisa A. REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                             2 KLLLKLLLKLLK 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                             4 KKLLKLLKKLLK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 KLLLKLLKLLK 13
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                                                                                                           Conservative
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83.3%;
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83.3%;
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                                                                                                        Score 40; DB Pred. No. 4.6; 0; Mismatches
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Pred. No.
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4.6;
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: MACINTOSH
COMPUTER: MACINTOSH
COMPUTER: MICROSOFT WORD, 4.0
CURRENT APPLICATION DATA:
APPLICATION UNMER: PCT/US94/07019
PRIOR APPLICATION DATA:
APPLICATION UNMER: 08/082,852
FILING DATE: JUNE 22, 1993
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
MOLECULE TYPE: peptide
PCT-US94-07019-3 Db Query Match 57.1%; Best Local Similarity 83.3%; Matches 10; Conservative 2 KILLKLLKKLK 13 | |||| ||| 5 KKILKLLKKLLK 16 Score 40; DB 5; Length 17; Pred. No. 4.6; 0; Mismatches 2; Indels 0; Gaps

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Search completed: June 17, 2002, 12:42:05 Job time: 225 sec